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OM nucleic - nucleic search, using sw model

Run on: October 12, 2004, 14:01:27 ; Search time 2154 Seconds

(without alignments) 12638.093 Million cell updates/sec

Title: US-09-996-128a-1

Perfect score: 6408

Sequence: 1 attccggcagatccagcac.....tcttatccaaaaacggaa 6408

Scoring table: IDENTITY_NUC

Gpop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : N_GenSeq_29Jan04:*

- 1: geneseqn1980s:*
- 2: geneseqn1990s:*
- 3: geneseqn2000s:*
- 4: geneseqn2001s:*
- 5: geneseqn2001s:*
- 6: geneseqn2002s:*
- 7: geneseqn2003s:*
- 8: geneseqn2003s:*
- 9: geneseqn2003s:*
- 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT 1

ID ABX10643 standard, DNA, 6408 BP.

XX

AC ABX10643;

XX

DT 22-APR-2003 (first entry)

XX

DE Vector, htyr-pING, containing human tyrosinase gene.

XX

HH human; gene; ds; melanoma; xenogeneic differentiation antigen; DA; PING;

KW

TYROSINASE; CANINE; GENE THERAPY; DOG; CYTOSTATIC.

XX

OS Homo sapiens.

XX

PN US2002150589-A1.

XX

PD 17-OCT-2002.

XX

PF 27-NOV-2001; 2001US-00996128.

XX

PR 10-DEC-1996; 96US-0032535P.

XX

PR 18-FEB-1997; 97US-0036419P.

XX

PR 10-DEC-1997; 97US-0036419P.

XX

PR 21-MAY-1999; 99US-00310897.

PR 26-JUN-2000; 2000US-0180651P.

XX

PR 28-JUL-2000; 2000US-00627694.

XX

PR (HOUG /) HOUGHTON A N.

XX

PR (BERG /) BERGMAN P J.

XX

PR (WOLC /) WOLCHOK J D.

XX

PR Houghton AN, Bergman PJ, Wolchok JD;

XX

PR WPI; 2003-182484/18.

XX

PR DR

XX

PR Treating melanoma in a mammalian subject comprises administering to the

XX

PT subject an immunological amount of a xenogeneic differentiation antigen

PT of the same type as a differentiation antigen expressed by melanoma cells

PT of the subject.

XX

PT Claim 26; Page 5-8; 15pp; English.

XX

CC The invention discloses a method for treating melanoma in a mammalian

CC subject which comprises administering to the subject an immunological

CC amount of a xenogeneic differentiation antigen (DA) of the same type as a

CC Aac86254 pgHRH-4 C

24 2008-6 31.3 5185 6 ABK53265 Growth ho
 25 2008-6 31.3 5188 4 Aac86265 Plasmid G
 26 2008-6 31.3 5188 4 ABK53277 Growth ho
 27 2008-6 31.3 5254 4 ABK8267 Plasmid P
 28 2008-6 31.3 5254 6 ABK85601 Growth ho
 29 2005-8 31.3 10447 9 ADE05454
 30 1993-8 31.1 10446 9 ADE05465
 31 1965-2 30.7 5299 7 AB55905
 32 1955-6 30.5 7528 4 AAF30156
 33 1942-2 30.3 5843 2 AAV00676
 34 1942-2 30.3 5245 7 AB55904
 35 1925-4 30.0 5888 2 AAV00677
 36 1922-6 29.9 2041 4 AAS60958
 37 1892-4 29.5 1894 2 AAO06552
 38 1890-8 29.5 1894 2 AAT01009
 39 1886-6 29.4 1964 7 ABP83843
 40 1886-6 29.4 1964 9 ADC09559
 41 1886-6 29.4 1984 2 AAT3316
 42 1886-6 29.4 2384 2 ABP76197
 43 1886-6 29.4 1906 2 AAO66548
 44 1885 29.4 1910 2 AAT35901
 45 1885 29.4 1910 2 AAT35901

ABK53265 Growth ho
 Aac86265 Plasmid G
 ABK53277 Growth ho
 ABK8267 Plasmid P
 ABK85601 Growth ho
 ADE05454 Vector PG
 ADE05465 Vector PG
 AB55905 DNA plasmid
 AAF30156 Bicistron
 AAV00676 DNA plasmid
 AB55904 DNA plasmid
 AAV00677 DNA plasmid
 AAS60958 Human can
 AAO6552 C1one BTR
 AAT01009 Human Tyr
 AAT75678 Human SK2
 ABP83843 Human Tyr
 ADC09559 Tyrosinas
 AAT3316 Tyrosinas
 ABP76197 Human tum
 AAO66548 Human tum
 AAT35901 Tyrosinas

CC DA expressed by melanoma cells of the subject. Also disclosed are pING vectors containing a sequence encoding the human or mouse tyrosinase genes. The methods and xenogeneic DA are useful for treating canine malignant melanoma (gene therapy) in dog suffering from the disease by administering an immunological amount of the xenogeneic DA and for other human tyrosinase gene.

Sequence 6408 BP: 1621 A: 1583 C: 1509 G: 1695 T: 0 U: 0 Other: 00

Query Match 100.0%; Score 6408; DB 7; Length 6408;

Best Local Similarity 100.0%; Pred. No: 0; Mismatches 0;

Matches 6408; Conservative 0; Gaps 0;

Indels 0; GCGCGCGAGG 1020

QY 1 ATTCCTCAGATATCCACACATGGCTGCGCCGCTGAGCTGAGG3CCGTTAACCCG 60

Db 1 ATTCCTCAGATATCCACACATGGCTGCGCCGCTGAGCTGAGG3CCGTTAACCCG 60

QY 61 CTGATCAGCCCTGACTGTGCTTCTAGTGGCACCATCTGTTGTTGCCCTCCCGT 120

Db 61 CTGATCAGCCCTGACTGTGCTTCTAGTGGCACCATCTGTTGTTGCCCTCCCGT 120

QY 121 GCCTTCCCTGACCCCTGGAGGTCCTCCACTGTGCTTCTCTAAATAAAATGAGGAAT 180

Db 121 GCCTTCCCTGACCCCTGGAGGTCCTCCACTGTGCTTCTCTAAATAAAATGAGGAAT 180

QY 181 TCCATGCCATGCTCTGAGTAGGTGCTATCTCGGGGATGGGAGCAG 240

Db 181 TCCATGCCATGCTCTGAGTAGGTGCTATCTCGGGGATGGGAGCAG 240

QY 241 CAGGGGGAGGATGGGAGACATAGCAGGATGGGGATGCAAGGGGGGGGGGG 300

Db 241 CAGGGGGAGGATGGGAGACATAGCAGGATGGGGATGCAAGGGGGGGGGGG 300

QY 301 CTGAGGCTCTGCCCTGCTGAGAGAACATACAGGATGGGGATGCAAGGGGGGGGG 360

Db 301 CTGAGGCTCTGCCCTGCTGAGAGAACATACAGGATGGGGATGCAAGGGGGGGGG 360

QY 361 ATCCACGCCAGAAAGTGGGGGACCACTGTGATGAGAGCTGGTGTAGGTGACCGTT 420

Db 361 ATCCACGCCAGAAAGTGGGGGACCACTGTGATGAGAGCTGGTGTAGGTGACCGTT 420

QY 421 GGTGATTTGAACTTTCTTCCACCGGAAACGGTCTCGGTGTCGGGAGAATGCGTGT 480

Db 421 GGTGATTTGAACTTTCTTCCACCGGAAACGGTCTCGGTGTCGGGAGAATGCGTGT 480

QY 481 CTGATCCTCAACTACGAAAGTTCGATTATTCACAAAGCCGGTCCGGTCAGTC 540

Db 481 CTGATCCTCAACTACGAAAGTTCGATTATTCACAAAGCCGGTCCGGTCAGTC 540

QY 541 ACCGTAATGCTCTGCCAGTGTACACCAATTACCAATTCTGATGAAACTCATCG 600

Db 541 ACCGTAATGCTCTGCCAGTGTACACCAATTACCAATTCTGATGAAACTCATCG 600

QY 601 AGCATCAATGAACTGCAATTATTATCATATCAGGATATTACATACATCCATTTCAAA 660

Db 601 AGCATCAATGAACTGCAATTATTATCATATCAGGATATTACATACATCCATTTCAAA 660

QY 661 AGCGTGTCTGPAATGAGGAGAAACTACCGAGGAGTTCATAGATGCAATATCC 720

Db 661 AGCGTGTCTGPAATGAGGAGAAACTACCGAGGAGTTCATAGATGCAATATCC 720

QY 721 TGGTACCGTCTGCCGATTCGACTCTGTCACACATTAATTCCCTCG 780

Db 721 TGGTACCGTCTGCCGATTCGACTCTGTCACACATTAATTCCCTCG 780

QY 781 TCAAATAAGGTATAGTCACTGAGAATCACCAGTGTGAGCTGAGTATCCGTGAGAT 840

Db 781 TCAAATAAGGTATAGTCACTGAGAATCACCAGTGTGAGCTGAGTATCCGTGAGAT 840

QY 841 GCGAAAGCTTATGCACTGCACTGAGGAGAAACTACCGAGGAGTTCATAGATGCA 900

Db 841 GCGAAAGCTTATGCACTGCACTGAGGAGAAACTACCGAGGAGTTCATAGATGCA 900

QY 901 TCAAATCACTGCAACCAACGTTATCATGGTATTGCGCTGAGGAGAGGA 960

Db 901 TCAAATCACTGCAACCAACGTTATCATGGTATTGCGCTGAGGAGAGGA 960

QY 961 ATATCGGATCCCTGTAAGAGACATTAACAAACAGGAATGCAACCGGCGAGG 1020

Db 961 ATATCGGATCCCTGTAAGAGACATTAACAAACAGGAATGCAACCGGCGAGG 1020

QY 1081 ATACATGCCAGGCATCACAACTTACCTGAACTGAGTATCTCTTAATACCTGG 1080

Db 1081 ATACATGCCAGGCATCACAACTTACCTGAACTGAGTATCTCTTAATACCTGG 1080

QY 1141 ATATCGCTGATGCTGCAAGAGGCAATTCGTCATGCACTAGGATTCATCTCA 1200

Db 1141 ATATCGCTGATGCTGCAAGAGGCAATTCGTCATGCACTAGGATTCATCTCA 1200

QY 1141 AAATGCTTCTGGGGAGTCAGGTGAGTGAACCATGTCATAGGATACCGATA 1200

Db 1141 AAATGCTTCTGGGGAGTCAGGTGAGTGAACCATGTCATAGGATACCGATA 1200

QY 1201 TCTGTAACATCTGGCACCTGAGGCTGACTGTTGAGGTTACATGCGCCAGTTAGCTCA 1260

Db 1201 TCTGTAACATCTGGCACCTGAGGCTGACTGTTGAGGTTACATGCGCCAGTTAGCTCA 1260

QY 1201 TCTGTAACATCTGGCACCTGAGGCTGACTGTTGAGGTTACATGCGCCAGTTAGCTCA 1260

Db 1201 TCTGTAACATCTGGCACCTGAGGCTGACTGTTGAGGTTACATGCGCCAGTTAGCTCA 1260

QY 1261 GCTTCCCATATACCGTACCTTGCCAGTTCAGAACACTCTGGCGCATCG 1320

Db 1261 GCTTCCCATATACCGTACCTTGCCAGTTCAGAACACTCTGGCGCATCG 1320

QY 1321 TTAATACCCATAAAATCAGCATCCATGTTGGATTAAATCAGGGCTGAGGAGGTT 1380

Db 1321 TTAATACCCATAAAATCAGCATCCATGTTGGATTAAATCAGGGCTGAGGAGGTT 1380

QY 1381 TCCCGTGTGATTTGCTCATAACCCCTGTTACTGTGTTATGAGCAGCT 1440

Db 1381 TCCCGTGTGATTTGCTCATAACCCCTGTTACTGTGTTATGAGCAGCT 1440

QY 1441 ATTTGTCATGAGATAATTATCTGTGAACTGACATCAGGATTGAGACAGTT 1500

Db 1441 ATTTGTCATGAGATAATTATCTGTGAACTGACATCAGGATTGAGACAGTT 1500

QY 1501 ATGGGGCTTCCCTCCCTCCCTGCAAGCTGCTTCTCTTCCCAACCCCAAG 1560

Db 1501 ATGGGGCTTCCCTCCCTCCCTGCAAGCTGCTTCTCTTCCCAACCCCAAG 1560

QY 1561 TGGGGTGAAGGCCAGGGCTGCGAGCAACCTCGGGAGGGCTGCGATAGCTC 1620

Db 1561 TGGGGTGAAGGCCAGGGCTGCGAGCAACCTCGGGAGGGCTGCGATAGCTC 1620

QY 1561 TGGGGTGAAGGCCAGGGCTGCGAGCAACCTCGGGAGGGCTGCGATAGCTC 1620

Db 1561 TGGGGTGAAGGCCAGGGCTGCGAGCAACCTCGGGAGGGCTGCGATAGCTC 1620

QY 1621 AGTTTACTCATATACTTTGATGTTAAACTCTATTATTTAAAGGATCA 1680

Db 1621 AGTTTACTCATATACTTTGATGTTAAACTCTATTATTTAAAGGATCA 1680

QY 1681 GGTGAGATCTTGTGATTAATCTCATGACCAAACTCCCTAACGGTGTGAGTTTGTC 1740

Db 1681 GGTGAGATCTTGTGATTAATCTCATGACCAAACTCCCTAACGGTGTGAGTTTGTC 1740

QY 1741 CTGAGGCTCAGGCCCTGATGAAAGATCAAGGATCTCTGAGTGTGAGTTTGTC 1800

Db 1741 CTGAGGCTCAGGCCCTGATGAAAGATCAAGGATCTCTGAGTGTGAGTTTGTC 1800

QY 1801 CTTAACTGCTCTGCAACAAACCCGGCTACCGAGGGTGTGCTGGG 1860

Db 1801 CTTAACTGCTCTGCAACAAACCCGGCTACCGAGGGTGTGCTGGG 1860

QY 1861 TCAAGAGCTTACACTCTTCTGGAAAGTCAAGGATCTCTGAGTGTGAGTTTGTC 1920

Db 1861 TCAAGAGCTTACACTCTTCTGGAAAGTCAAGGATCTCTGAGTGTGAGTTTGTC 1920

QY 1921 TACTGTTCTCTGAGTGTGAGCTGAGGCTTACAGAACCTCTGTGAGCTGAGC 1980

Db 1921 TACTGTTCTCTGAGTGTGAGCTGAGGCTTACAGAACCTCTGTGAGCTGAGC 1980

QY 1981 TACTGTTCTCTGAGTGTGAGCTGAGGCTTACAGAACCTCTGTGAGCTGAGC 1980

RESULT 2				
ABX10644	ABX10644 standard, DNA, 6485 BP.	QY	121	GCCTCTTGACCCCTGAGGGGCCACTCCCTGCTCTTCTTAATAAGGAAAT 180
ID			121	
XX			121	GCCTCTTGACCTGAGGGCCACTCCCTGCTCTTCTTAATAAGGAAAT 180
AC			181	TGCAATCGCATTTGCTGAGTAGGTCATCTAATCTGGGGCTGGGGCTGGGAGAC 240
XX			181	
ABX10644;			241	CAGGGGGAGGATTTGGAGAGACATAGAGGATCTGAGGATGGGATGAGGAAAT 300
DT	22-APR-2003 (first entry)		241	
XX	Vector, hytr-PING, containing mouse tyrosinase gene.		301	CTGAGGCTCTGCTGTGAGAGAGACATAGAGGATGAGGATGGGATGAGGAAAT 360
DE			301	
XX	Mouse; gene; ds; melanoma; xenogeneic differentiation antigen; DA; PING;		361	ATCCAGCCAGAAAGTGAGGGAGCACGGGTGAGGAGACCTTGTGAGGACAGT 420
KW	tyrosinase; canine; gene therapy; dog; cytostatic.		361	
XX			421	ATCCAGCCAGAAAGTGAGGGAGCACGGGTGAGGAGACCTTGTGAGGACAGT 420
OS	Mus sp.		421	
XX			481	CTGATCCTTCACACTCAGAAAGTCAGTTCGATACACCGCTGATGCCCATC 360
PN	US2002150589-A1.		481	
XX			481	CTGATCCTTCACACTCAGAAAGTCAGTTCGATACACCGCTGATGCCCATC 360
PD	17-OCT-2002.		481	CTGATCCTTCACACTCAGAAAGTCAGTTCGATACACCGCTGATGCCCATC 360
XX			481	CTGATCCTTCACACTCAGAAAGTCAGTTCGATACACCGCTGATGCCCATC 360
PR	27-NOV-2001; 2001US-00996128.		481	CTGATCCTTCACACTCAGAAAGTCAGTTCGATACACCGCTGATGCCCATC 360
PR	10-DEC-1996; 96US-00322535P.		481	CTGATCCTTCACACTCAGAAAGTCAGTTCGATACACCGCTGATGCCCATC 360
PR	18-FEB-1997; 97US-00361619P.		540	CTGATCCTTCACACTCAGAAAGTCAGTTCGATACACCGCTGATGCCCATC 540
PR	10-DEC-1997; 97NO-05022669.		540	CTGATCCTTCACACTCAGAAAGTCAGTTCGATACACCGCTGATGCCCATC 540
PR	21-MAY-1999; 99US-00308697.		541	AGCCTAATGCTCTGCCAGGTGAGGACCTTCCACCGGAACTCTGGGTGAT 600
PR	26-JAN-2000; 2000US-0180651P.		541	AGCCTAATGCTCTGCCAGGTGAGGACCTTCCACCGGAACTCTGGGTGAT 600
PR	28-JUL-2000; 2000US-006227694.		541	AGCCTAATGCTCTGCCAGGTGAGGACCTTCCACCGGAACTCTGGGTGAT 600
PA	(HOUG/) BURGESS A. N.		601	AGCCTAATGCTCTGCCAGGTGAGGACCTTCCACCGGAACTCTGGGTGAT 600
PA	(BERG/) BERGMAN P. J.		601	AGCCTAATGCTCTGCCAGGTGAGGACCTTCCACCGGAACTCTGGGTGAT 600
PA	(WOLC/) WOLCHOK J. D.		660	AGCCTAATGCTCTGCCAGGTGAGGACCTTCCACCGGAACTCTGGGTGAT 660
XX			661	AGCGTTCTGGATAAACCTACCGGAGCTTCCACAGATTCGAGATCC 720
PT	Houghton AN, Bergman PJ, Wolchok JD,		661	AGCGTTCTGGATAAACCTACCGGAGCTTCCACAGATTCGAGATCC 720
DR			661	AGCGTTCTGGATAAACCTACCGGAGCTTCCACAGATTCGAGATCC 720
XX			721	TGGTATCGCTCTGGGATTCGACTTCAGTTCGTCACATCACTATACACCTATTATTCGGAGATCC 780
PT	Treating melanoma in a mammalian subject an immunological amount of a xenogeneic differentiation antigen of the same type as a		721	TGGTATCGCTCTGGGATTCGACTTCAGTTCGTCACATCACTATACACCTATTATTCGGAGATCC 780
PT	vector containing a sequence encoding the human or mouse tyrosinase genes. The methods and xenogeneic DA are useful for treating canine malignant melanoma (gene therapy) in dog suffering from the disease by administering an immunological amount of the xenogeneic DA and for other mammals. The sequence presented is the vector, hytr-PING, containing the mouse tyrosinase gene		781	TCAAATCTCGATCACCAAACCGTTATCATCGTGAATGGCGCTGAGGAGACCA 960
XX			781	TCAAATCTCGATCACCAAACCGTTATCATCGTGAATGGCGCTGAGGAGACCA 960
PS	Claim 27; Page 8-11; 15pp; English.		781	TCAAATCTCGATCACCAAACCGTTATCATCGTGAATGGCGCTGAGGAGACCA 960
XX			840	GCCTCTTGACCCCTGAGGGGCCACTCCCTGCTCTTCTTAATAAGGAAAT 180
CC	The invention discloses a method for treating melanoma in a mammalian subject which comprises administering to the subject an immunological amount of a xenogeneic differentiation antigen (DA) of the same type as a		840	GCCTCTTGACCCCTGAGGGGCCACTCCCTGCTCTTCTTAATAAGGAAAT 180
CC	DA expressed by melanoma cells of the subject. Also disclosed are PING vectors containing a sequence encoding the human or mouse tyrosinase genes. The methods and xenogeneic DA are useful for treating canine malignant melanoma (gene therapy) in dog suffering from the disease by administering an immunological amount of the xenogeneic DA and for other mammals. The sequence presented is the vector, hytr-PING, containing the mouse tyrosinase gene		840	GCCTCTTGACCCCTGAGGGGCCACTCCCTGCTCTTCTTAATAAGGAAAT 180
CC	Sequence 6485 BP; 1658 A; 1570 C; 1504 G; 1753 T; 0 U; 0 Other;		841	GCCTCTTGACCCCTGAGGGGCCACTCCCTGCTCTTCTTAATAAGGAAAT 180
SQ	Query Match 88 0%; Score 5636; DB 7; Length 6485;		841	GCCTCTTGACCCCTGAGGGGCCACTCCCTGCTCTTCTTAATAAGGAAAT 180
Best Local Similarity 94.8%; Pred. No. 0; Mismatches 5884; Conservative 0; Mismatches 270; Indels 56; Gaps 3;			841	GCCTCTTGACCCCTGAGGGGCCACTCCCTGCTCTTCTTAATAAGGAAAT 180
QY	1 ATTCGCAAGATTCAGCACTGCGCGCGCTCGAGCTAGGCTAGGGCCGTTAACCGG 60		901	TCAAATCTCGATCACCAAACCGTTATCATCGTGAATGGCGCTGAGGAGACCA 960
QY	1 ATTCGCAAGATTCAGCACTGCGCGCGCTCGAGCTAGGCTAGGGCCGTTAACCGG 60		901	TCAAATCTCGATCACCAAACCGTTATCATCGTGAATGGCGCTGAGGAGACCA 960
Db	CTGATCAGCTCGACTGTGCTCTCGAGTTCAGGATCCACATCTGTTGCGCTTCCCCCT 120		961	ATATCGCGATGCTGTTAACGGAACTTACAAACAGGATCATGACCGCCGAGG 1020
Db	CTGATCAGCTCGACTGTGCTCTCGAGTTCAGGATCCACATCTGTTGCGCTTCCCCCT 120		961	ATATCGCGATGCTGTTAACGGAACTTACAAACAGGATCATGACCGCCGAGG 1020
Db	CTGATCAGCTCGACTGTGCTCTCGAGTTCAGGATCCACATCTGTTGCGCTTCCCCCT 120		1081	ATACCTGTTTCCGGGAACTCGAGTGGAGACATCATCAGGATGAGGATCGGATA 1140
Db	ATTCGCAAGATTCAGCACTGCGCGCGCTCGAGCTAGGCTAGGGCCGTTAACCGG 60		1081	ATACCTGTTTCCGGGAACTCGAGTGGAGACATCATCAGGATGAGGATCGGATA 1140
Db	ATACCTGCGATGCTGCTCTCGAGTTCAGGATCCACATCTGTTGCGCTTCCCCCT 120		1141	ATATCGCTGTTGGAGAGGGATAATTCTGTCAGGCAATTAGCTGAGCATCTCA 1200
Db	ATACCTGCGATGCTGCTCTCGAGTTCAGGATCCACATCTGTTGCGCTTCCCCCT 120		1141	ATATCGCTGTTGGAGAGGGATAATTCTGTCAGGATGAGGATGAGGATCGGATCTCA 1200

Db	1201	TCGTAAQATCATGGCAGCTACCTTGGCACTGTTCAAGAAGAACACTCTGGCATCG	1260	Db	2281	GTATCTTATAGTCCTGCGGTTGCCACCTCTGACTTGAGGTCGATTTGGATG	2340
Qy	1261	GGCTTCCATACATCATGATAGATGTCGACCTGATGCCACATTATCGGGAGCCAT	1320	Qy	2341	CGCGTCGGGGGGGGGGCCATTGGAAGAACCCACGCCAACCGGGCTTTACG3TCT	2400
Db	1261	GGCTTCCATACATCATGATAGATGTCGACCTGATGCCACATTATCGGGAGCCAT	1320	Db	2341	CTCGTCAGGGGGGGGGCCATTGGAAGAACCCACGCCAACCGGGCTTTACG3TCT	2400
Qy	1321	TTATACCATTAATCAGCATCATGTTGAAATTATCGGGCTCGAGGAGAGTT	1380	Qy	2401	GGCTTTCGCGCTTTCGACATGTTCTTCGCGTATCCCTGATCTGIGGA	2460
Db	1321	TTATACCATTAATCAGCATCATGTTGAAATTATCGGGCTCGAGGAGAGTT	1380	Db	2401	GGCTTTCGCGCTTTCGACATGTTCTTCGCGTATCCCTGATCTGIGGA	2460
Qy	1381	TCGGTGAATATGGCTATACACCCCTTGTATTACTGTTATGAGACAGTT	1440	Qy	2461	TRACCGTATTACGCCATGATTAGTATAGPATCATTCAGGG3CATAGTC	2520
Db	1381	TCGGTGAATATGGCTATACACCCCTTGTATTACTGTTATGAGACAGTT	1440	Db	2461	TRACCGTATTACGCCATGATTAGTATAGPATCATTCAGGG3CATAGTC	2520
Qy	1441	ATGTTCATGATGATGATATTTATCTGCACTGACATCAGAGATTTGAGACAGTT	1500	Qy	2521	ATAGCCATATGGAGTCGGTACATACTAGGTAATGGGCTGGTAC	2580
Db	1441	ATGTTCATGATGATGATATTTATCTGCACTGACATCAGAGATTTGAGACAGTT	1500	Db	2521	ATAGCCATATGGAGTCGGTACATACTAGGTAATGGGCTGGTAC	2580
Qy	1501	ACCTGGCTTCCCCCCCCCTCAGGTTCTCCATTCCACCCACCCCCAG	1560	Qy	2580	CGCCCAAGACCCCGCCATGACCTCAATATGAGGAGCTATAGTGACAG	2640
Db	1501	ACCTGGCTTCCCCCCCCCTCAGGTTCTCCATTCCACCCACCCCCAG	1560	Db	2581	CGCCCAAGACCCCGCCATGACCTCAATATGAGGAGCTATAGTGACAG	2640
Qy	1561	TCGGTGAAGGCCAGGGCTCCAGCCAGCGGGGGGAGGGCGAGCC	1620	Qy	2641	GATATGGCTATATGCCATAGAGCGACATCAAGTGCACATGCCATAGCTC	2700
Db	1561	TCGGTGAAGGCCAGGGCTCCAGCCAGCGGGGGAGGGCGAGCC	1620	Db	2641	GATATGGCTATATGCCATAGAGCGACATCAAGTGCACATGCCATAGCTC	2700
Qy	1621	AGCTTACTCATATACTTTAGTTAGTTAAACTCTATTAAATTAAAGGCTA	1680	Qy	2701	GATCTATACATGAAATATGGCATAGCCATATAGCTATGTTATAGCTA	2760
Db	1621	AGCTTACTCATATACTTTAGTTAGTTAAACTCTATTAAATTAAAGGCTA	1680	Db	2701	GATCTATACATGAAATATGGCATAGCCATATAGCTATGTTATAGCTA	2760
Qy	1681	GGTGAAGATCTTTGATACTCAGACAAATCCCTAACGGTTTCGTTCA	1740	Qy	2760	ATACATATTGGCTATGGCATATGCTAACAGTGTATCTATCATATGTCATTA	2820
Db	1681	GGTGAAGATCTTTGATACTCAGACAAATCCCTAACGGTTTCGTTCA	1740	Db	2761	ATACATATTGGCTATGGCATATGCTAACAGTGTATCTATCATATGTCATTA	2820
Qy	1741	CTAGCGTCAGACCCCGTAGAAAGATAAAAGGATCTCTTGAGATCCTTTCG	1800	Qy	2821	TATGGTCATGCCATTATGACCGCATGTCGACATGTGATATGACTTATPATA	2880
Db	1741	CTAGCGTCAGACCCCGTAGAAAGATAAAAGGATCTCTTGAGATCCTTTCG	1800	Db	2821	TATGGTCATGCCATTATGACCGCATGTCGACATGTGATATGACTTATPATA	2880
Qy	1801	CGTATCTGCTGCTGCAACAAACAAACACCGCTTACAGCGAGTGTGTTGCGGA	1860	Qy	2881	GTATCATTAAGGGCATAGTGTATAGCCATTATGGAGTTCGGTACATACT	2940
Db	1801	CGTATCTGCTGCTGCAACAAACACCGCTTACAGCGAGTGTGTTGCGGA	1860	Db	2881	GTATCATTAAGGGCATAGTGTCTAGCCATTATGGAGTTCGGTACATACT	2940
Qy	1861	TCAGAGCTTACCAACTCTTTCGAAAGGTACTGGCTTCAAGAGGAGATACAA	1920	Qy	2941	TACGGTAATGGCCGGCTGGTGAAGGCCAACAGGACCCGCCATTGACTCATGAT	3000
Db	1861	TCAGAGCTTACCAACTCTTTCGAAAGGTACTGGCTTCAAGAGGAGATACAA	1920	Db	2941	TACGGTAATGGCCGGCTGGTGAAGGCCAACAGGACCCGCCATTGACTCATGAT	3000
Qy	1921	TATGTTCTTCTAGTGGCGTAGTGGCCACACTTCAAGACTCTGAGCC	1980	Qy	3001	GACGTATGTCCTACATACACCCAAATAGGACTCTTCATGAGCGCAATGGGTGAGTA	3060
Db	1921	TATGTTCTTCTAGTGGCGTAGTGGCCACACTTCAAGACTCTGAGCC	1980	Db	3001	GACGTATGTCCTACATACACCCAAATAGGACTCTTCATGAGCGCAATGGGTGAGTA	3060
Qy	1981	TACATACCTGCTGCTGCTAATCCCTGTTACCGAGTGGCCAGTGTGCG	2040	Qy	3061	TTACCGTAACTGGCCACCTGGCAGTACATCAAGTGTATATGCCAAGTCCGCCCC	3120
Db	1981	TACATACCTGCTGCTGCTAATCCCTGTTACCGAGTGGCTGCGAGTGTG	2040	Db	3061	TTACCGTAACTGGCCACCTGGCAGTACATCAAGTGTATATGCCAAGTCCGCCCC	3120
Qy	2041	TCTTACCCGGTGGACTCAAGACGATAGTACCGGATAAGGCCAGGGCTGGCTGAC	2100	Qy	3121	TATGACTCAAGACGCTAATGGCGCGCTGGCATATGCCAGTACATGACCT	3180
Db	2041	TCTTACCCGGTGGACTCAAGACGATAGTACCGGATAAGGCCAGGGCTGGCTGAC	2100	Db	3121	TATGACTCAAGACGCTAATGGCGCGCTGGCATATGCCAGTACATGACCT	3180
Qy	2101	GGGGGGTGTGGCAACACCCGACTGGAGCGACGACTACCGGACTGAGACT	2160	Qy	3181	GGACTTCTACTGGCAGTACATCAAGTGTATGGCTATGGCTGAGTGGCG	3240
Db	2101	GGGGGGTGTGGCAACACCCGACTGGAGCGACGACTACCGGACTGAGACT	2160	Db	3181	GGACTTCTACTGGCAGTACATCAAGTGTATGGCTATGGCTGAGTGGCG	3240
Qy	2161	ACAGCGTGTGAGCTATGAGAGAGCGCAGCTTCCGAAGGGAGGAGCTGCC	2220	Qy	3241	GTTCGGAGTACACCATGGCGTGTGACTACGGGTTGACTCACGGGATTCGAAGCT	3300
Db	2161	ACAGCGTGTGAGCTATGAGAGAGCGCAGCTTCCGAAGGGAGGAGCTGCC	2220	Db	3241	GTTCGGAGTACACCATGGCGTGTGACTACGGGTTGACTCACGGGATTCGAAGCT	3300
Qy	2221	GGTAAAGCGCAGGAGCTGGCAACAGAGGAGCTTCAGGGGAAACGCTG	2280	Qy	3301	CCACCCCATGAGCTGTGGAGTTGGCAACATCAAGGGACTTCGAAGCT	3360
Db	2221	GGTAAAGCGCAGGAGCTGGCAACAGAGGAGCTTCAGGGGAAACGCTG	2280	Qy	3361	ATGTCGATAACCCCGCCCGTGAAGCAATGGGGTAGGGTACGGTGGAGGT	3420
Qy	2281	GTATCTTATAGTCCTGCGGTTGCCACCTCTGACTTGAGGTCGATTTGGATG	2340	Db	3361	ATGTCGATAACCCCGCCCGTGAAGCAATGGGGTAGGGTACGGTGGAGGT	3420

QY	3421	CTATATAAGGAGACTCGTTAGTGAAACCGTCAGATCGCCTGGAGACSCCATCCACGCTG	3480	QY	4501	GGATTCCCGGA-----ACAA 4516
Db	3421	CTATATAAGGAGACTCGTTAGTGAAACCGTCAGATCGCCTGGAGACSCCATCCACGCTG	3480	Db	4501	GGATTCTGTGACCTATTAACCTATTTGCGAGATTGATGATGATAAAGGAGAAA 4560
QY	3481	TTTGACTTCATAGAAGACCGGACCGATCGCCTCCGGCGCCGGAAACCGTGT	3540	QY	4517	TGCTCCCTGCTGTTGACTGCTGCTGCTGAGGTTCCAGACCTCGCTGGCCATTC 4576
Db	3481	TTTGACTTCATAGAAGACCGGACCGATCGCCTCCGGCGCCGGAAACCGTGT	3540	Db	4561	TGTTCTGCTGTTGACTGCTGCTGCTGAGGTTCCAGACCTCGCTGGAGTTTCAGATCTCTG 4620
QY	3541	TGGAGCGGGATTCCCGTGCCAAAGAGTGCGTAGTGAAGTACCGCTTATAGACATAGAGCA	3600	QY	4577	CTAGAGCTGTGCTCTAAGACCTGATGGAGAGGAACCTGTCACCGTGGAGG 4636
Db	3541	TGGAGCGGGATTCCCGTGCCAAAGAGTGCGTAGTGAAGTACCGCTTATAGACATAGAGCA	3600	Db	4621	CTCGAGCCGTGCTCTAAGACCTGTTGCGCTTACCGTGGAGG 4680
QY	3601	CACCCCTTGCTCTATGATGCTATGCTTGGCTTGCGCTTACACCCCGCG	3660	QY	4637	GGGACAGGAGTCCCTGCGCCAGCTTCAGGAGAGGAACTGTCACCGTGGAGG 4696
Db	3601	CACCCCTTGCTCTATGATGCTTGGCTTGCGCTTACACCCCGCG	3660	Db	4681	GTGATGGAGTCCCTGCGCCAGCTTCAGGAGAGGAACTGTCACCGTGGAGG 4720
QY	3661	TCCCTATGCTATAGGTGAGGTATAGCTAGCTATAGCTATAGGTGAGGTTAGGATAT	3720	QY	4697	CCATGACCACTTGGCTCAATTCCCTACAGGGTGTGAGGAACTGTCACCGTGGAGG 4756
Db	3661	TCCCTATGCTATAGGTGAGGTATAGCTAGCTATAGGTGAGGTTAGGATAT	3720	Db	4741	CCATGACCACTTGGCTCAATTCCCTACAGGGTGTGAGGAACTGTCACCGTGGAGG 4800
QY	3721	TGACCACTCCCTATTTGTCAGCTACTTTCATTAACACMGGCTTTC	3780	QY	4757	CTTCGCTCTTATAAGGACCTGCGACTCTGCTGCAACTCATGGATTCAGCT 4816
Db	3721	TGACCACTCCCTATTTGTCAGCTACTTTCATTAACACMGGCTTTC	3780	Db	4801	CCCTGTGTTATAAGGACCTGCGACTCTGCTGCAACTCATGGATTCAGCT 4860
QY	3781	CACAACTATCTATTTGCTATGCTTACCTCTGCTCTCAGACTGACAGGGACT	3840	QY	4817	GAAACTGCAAGTGGTGGCTTTCAGGAGAGGAACTGCAAGAGAGGAACTGTCACCGTGGAGG 4876
Db	3781	CACAACTATCTATTTGCTATGCTTACCTCTGCTCTCAGACTGACAGGGACT	3840	Db	4861	GAAACTGTAAGTTGGATTGGGGCCAAATGTCAGAGAAAGGAGCTTGTGATTAGA 4920
QY	3841	TGATTTTACAGATGGCTCCATTATTATTTACAAATTGACATACAAACGCC	3900	QY	4877	GAAACATCTGTTGAGGACCTGCGACTCTGCTGCAACTCATGGATTCAGCT 4936
Db	3841	TGATTTTACAGATGGCTCCATTATTATTTACAAATTGACATACAAACGCC	3900	Db	4921	GAAACATTTTGTGAGTGTCTCCGAAGAAATAAGTCTGAGGAACTGTCAGTGTGCTCAGGAACTG 4980
QY	3901	GTCCCCCGTCCGGCAAGTTTAACTAACTAGCTGGCTCTCACGGAACTCGGT	3960	QY	4937	CAAGCATACCATCAGCTGAGACTATCCCAAGGAACTGACAGAGAGGAACTGTCACCGTGGAGGACTCTG 4996
Db	3901	GTCCCCCGTCCGGCAAGTTTAACTAACTAGCTGGCTCTCACGGAACTCGGT	3960	Db	4981	CAAAACATACATCAGCTCAGTCTATGTCATCCCAAGGAACTGACAGGAACTGAC 5040
QY	3961	ACGTTTCCGACATGGCTTCTCCGGAGCTTCCACATCCGGCCCTCTG	4020	QY	4997	ATGGATCACACCATGTTAACGACATCAATTATGACCTCTTCTCTGATGCACT 5056
Db	3961	ACGTTTCCGACATGGCTTCTCCGGAGCTTCCACATCCGGCCCTCTG	4020	Db	5041	ATGGGTCAACACCATGTTAACGACATCACTCTGAGGAACTGACAGGAACTGAC 5100
QY	3960	ACGTTTCCGACATGGCTTCTCCGGAGCTTCCACATCCGGCCCTCTG	4020	QY	5057	ATATGTCATGGATGCTGACTGTTGGGAGATGAACTGAGGAGCATGATGTTG 5116
Db	3960	ACGTTTCCGACATGGCTTCTCCGGAGCTTCCACATCCGGCCCTCTG	4020	Db	5101	ATCATGTCACGGACACACTGCTTGGGGCTCTGAAATATGAGGAACTGAC 5160
QY	4021	TCCCATGCCCCACGGCTTATGTCGCTGGAGCTCTGCTCTAACGAGGSC	4080	QY	5117	CCCTGAAACCCGGCTTCTGCTTGGCATAGACATCTCTGTTGGAGAACAG 5176
Db	4021	TCCCATGCCCCACGGCTTATGTCGCTGGAGCTCTGCTCTAACGAGGSC	4080	Db	5161	CCCATGAAACCCGGCTTCTGCTTGGCATAGACATCTCTGTTGGAGAACAG 5220
QY	4081	AGACITTAGGGACAGACAATGCCAACACCAACGACATGGCTGGAGA	4140	QY	5177	AAATCCGAGAGCTGACGGAGATGAAACTCACTATCCATATTGGACTGCGGATG 5236
Db	4081	AGACITTAGGGACAGACAATGCCAACACCAACGACATGGCTGGAGA	4140	Db	5221	AAATCCGAGAGCTAATGCTGAGGAACTGACATCTCTGTTGGAGAACAG 5280
QY	4141	GGGTATGTCGCTGAAATGAGCTCGAGATGGCTGGAGATGAGA	4200	QY	5237	CAGAAAGTGTGACATGTCAGATAGTACAGATAGTACATGGAGGGTCTGCAACCCACAAATCTA 5296
Db	4141	GGGTATGTCGCTGAAATGAGCTCGAGATGGCTGGAGATGAGA	4200	Db	5281	CAGAAAGTGTGACATGTCAGATAGTACAGATAGTACATGGAGGGTCTGCAACCCACAAATCTA 5340
QY	4201	CTTAAAGGCCGGAGAGAGATGGCTGGAGGAGCTGAGTGTGAGGAG	4260	QY	5297	ACTTACTCGCCCGCCATCTTCTCTCTGGAGATGCTGAGGCGATGAGG 5356
Db	4201	CTTAAAGGCCGGAGAGAGATGGCTGGAGGAGCTGAGTGTGAGGAG	4260	Db	5341	ACTTACTCGCCCGCCATCTTCTCTCTGGAGATGCTGAGGCGATGAGG 5400
QY	4261	GAGGAACTCCGGTGCGCTGTAACCGTGGAGGAGCTGAGTGTGAGGAG	4320	QY	5357	AGTACACAGGCCATCGCTTATGCAATGCAAGCGCGAGGGACCTTACGGCTGATC 5416
Db	4261	GAGGAACTCCGGTGCGCTGTAACCGTGGAGGAGCTGAGTGTGAGGAG	4320	Db	5401	AGTATATGACCATGAGCTTATGCGATGAGACACTGGGGACCTTACGGCTG 5460
QY	4321	ATGGCTGCCCCGGCGCCACAGACATATAAGCTACAGCTAAGGAGACCA	4380	QY	5417	CTGGAAACCATGACAATCCGAGACCAAGGGCTCCCTCTGAGCTGAGAATT 5476
Db	4321	ATGGCTGCCCCGGCGCCACAGACATATAAGCTACAGCTAAGGAGACCA	4380	Db	5461	CTGGAAACCATGACAATCCGAGACCAAGGGCTCCCTCTGAGCTGAGAATT 5520
QY	4381	ATGGCTGCCCCGGTGCGCTGTAACCTAACGCTGAGGAGCTGAGTGTGAGGACCA	4440	QY	5477	GCTGAGTGTGACCAATGCTGAGGAAAGTGCCTAACCTGAGCTTA 5536
Db	4381	ATGGCTGCCCCGGTGCGCTGTAACCTAACGCTGAGGAGCTGAGTGTGAGGACCA	4440	Db	5521	GTCGAGTGTGACCAATGCTGAGGAAAGTGCCTAACCTGAGCTTA 5580
QY	4441	GCTGAGTGTGACCAATGCTGAGGAGCTGAGTGTGAGGAGCTGAGTGTGAGGACCA	4500	QY	5537	GAATACACTGGAGGATTGCTGACTACTACTGGAGATGGGATAGGGATGGCTCAAGCA 5596

QY	1065	TTCTTCTATACTCTGGAATGTCGTTTCCGGGGATCCAGTGGAGCTAACATGCACT	1124	Db
Db	4901	TTCTTCTATACTCTGGAATGTCGTTTCCGGGGATTCGGAGGATCGCAGTGGAGCTAACATGCACT	4842	QY
QY	1125	ATCAGGACTACGATAAAATGCTGATGCTGAGGACATAATTGTCAGCCAGT	1184	Db
Db	4841	ATCAGGACTACGATAAAATGCTGATGCTGAGGACATAATTGTCAGCCAGT	4782	QY
QY	1185	TAGCTGACCATCTCTGTAACATCATGGCAACGCTACTTGCAGAA	1244	Db
Db	4721	CAACTCTGGCGCATGGCTCCCATACATGGCAACGCTACTTGCAGAA	4722	QY
QY	4781	TAGCTGACCATCTCTGTAACATCATGGCAACGCTACTTGCAGAA	4722	Db
QY	1305	ATTATCGAGGCCATTATACCCATAAAATGAGCATCTGTTGAGG	1364	Db
Db	4661	ATTATCGAGGCCATTATACCCATAAAATGAGCATCTGTTGAGG	4602	QY
QY	1245	CAACTCTGGCGCATGGCTCCCATACATGGCAACGCTACTTGCAGAA	1304	Db
Db	4721	CAACTCTGGCGCATGGCTCCCATACATGGCAACGCTACTTGCAGAA	4662	QY
QY	4781	TAGCTGACCATCTCTGTAACATCATGGCAACGCTACTTGCAGAA	4722	Db
QY	1365	CCTCGAGCAGAGCTTCCCGTCAATGGCTCAAGACCCCTGTTAC	1424	Db
Db	4601	CCTCGAGCAGAGCTTCCCGTCAATGGCTCAAGACCCCTGTTAC	4542	QY
QY	1425	GTAAGCAGACAGTTATGTCATGATGATATATTATCTGTGCAATGTA	1484	Db
Db	4541	GTAAGCAGACAGTTATGTCATGATGATATATTATCTGTGCAATGTA	4521	QY
QY	1485	GAGATTGAGACAAAGGGCCTTCCCCCCCCGTCAGSGTTTCCUTTCC	1544	Db
Db	4520	GAGATTGAGACAAAGGGCCTTCCCCCCCCGTCAGSGTTTCCUTTCC	4521	QY
QY	1605	GCCCTGCATAGCCTCAGTTACTCTATACTTTAGATTGATTAAACTCT	1664	Db
Db	4520	GCCCTGCATAGCCTCAGTTACTCTATACTTTAGATTGATTAAACTCT	4521	QY
QY	1545	CACCCACCCCCAAGTTGGGTAAGGCCAGGGCTCCAGGCCACGTGGGGAG	1604	Db
Db	4520	CACCCACCCCCAAGTTGGGTAAGGCCAGGGCTCCAGGCCACGTGGGGAG	4521	QY
QY	1665	AATTAAAGGATCTAGGAGATCCTTTGATAATCTCATGACCAAAATCCTAAC	1724	Db
Db	4520	AATTAAAGGATCTAGGAGATCCTTTGATAATCTCATGACCAAAATCCTAAC	4500	QY
QY	1725	GTGAGTTTGTGTCACGTAGCGCTAGACCCCGTGAAGAAAGATCAAGGATCTTGTGAG	1784	Db
Db	4499	GTGAGTTTGTGTCACGTAGCGCTAGACCCCGTGAAGAAAGATCAAGGATCTTGTGAG	4440	QY
QY	1785	ATCCTTTTCTGGCGTAATCTGCTGTGCAACAAAAACACCGCTACCGCG	1844	Db
Db	4439	ATCCTTTTCTGGCGTAATCTGCTGTGCAACAAAAACACCGCTACCGCG	4380	QY
QY	1845	TGCTTGTGTCACGTAGCGCTACRACTCTTTCGAGGTACTGGCTCACCA	1904	Db
Db	4379	TGCTTGTGTCACGTAGCGCTACRACTCTTTCGAGGTACTGGCTCACCA	4320	QY
QY	1905	GACCGAGTACCAATCTGTCAGGCGTAGTTAGGCCACCACTCAAGA	1964	Db
Db	4319	GACCGAGTACCAATCTGTCAGGCGTAGTTAGGCCACCACTCAAGA	4360	QY
QY	1965	ACTCTGAGCACCCTCATACCTCGCTCTGCAATCTGTAACAGTG---GCTGCTG	2021	Db
Db	4259	ACTCTGAGCACCCTCATACCTCGCTCTGCAATCTGTAACAGTG---GCTGCTG	4200	QY
QY	2022	CCAGTGGCGATAACTCTGTCCTACCGGGTGTGACTCAAGCAAGTACCGCT	2081	Db
QY	4139	CCAGTGGCGATAACTCTGTCCTACCGGGTGTGACTCAAGCAAGTACCGCT	4140	Db
QY	4139	CCAGTGGCGATAACTCTGTCCTACCGGGTGTGACTCAAGCAAGTACCGCT	4080	Db
QY	2142	ACACCGACTGAGATACTTAAAGCTGAGCTATGAGAACGCCAGCTCCGGAGGA	2201	Db
Db	4079	ACACCGACTGAGATACTTAAAGCTGAGCTATGAGAACGCCAGCTCCGGAGGA	4020	QY
QY	2202	GAAGGGGGAGGATTCGGTAAAGGGAGGTATGAGAACGCCAGCTCCGGAGGA	2261	Db
Db	4019	GAACCGGGAGGATTCGGTAAAGGGAGGTATGAGAACGCCAGCTCCGGAGGA	3960	QY
QY	2262	TCCAGGGGAAAGGCCTGATCTTATGAGCTCTGGCTCTGGCTGCACTCTGACTG	2321	Db
Db	3959	TCCAGGGGAAAGGCCTGATCTTATGAGCTCTGGCTGCACTCTGACTG	3900	QY
QY	2322	ACCGTGGATTTGATCCCGTCAAGGGAGGCTATGAGAACGCCAGCTCCGGAGGA	2381	Db
Db	3899	ACGCPGATTTCTGATGCTGTCAGGGGGCGAGCTATGAGAACGCCAGCAACG	3840	QY
QY	2382	GGCCTTTTAAGGTCTCGGCTTGTGCTGAGCTACAGCTTCTGCGT	2441	Db
Db	3839	GGCCTTTTAAGGTCTCGGCTTGTGCTGAGCTACAGCTTCTGCGT	3780	QY
QY	2442	TATCCCTGATCTCTGATGCTGAGCTACCGCC-ATGCTTATGATGATAC	2500	Db
Db	3779	TATCCCTGATCTCTGATGCTGAGCTACCGCTTGTGAGCTGATACCGCTGCG	3720	QY
QY	2501	ATTCAGGGCTATAGTCATAGCCATATGGAGTCCGGTACATAC--TTAC	2557	Db
Db	3719	ATTCAGGGCTATAGTCATAGCCATATGGAGTCCGGTACATAC--TTAC	3660	QY
QY	2558	GTTAAATGGCCCGCTGGCTGACCCCAAGGACCCCGCCATGACGTCATAATGAC	2617	Db
Db	3659	GAAACCGCTCTCCCGCGTGGCGATCATATGAGCTGAGCAACAGGTT	3600	QY
QY	2618	GAGATCTGATATAGTCAGCACTATGGCTGAGCTGAGCTGAGCAACAGGTT	2677	Db
Db	3539	GAGATCTGATATAGTCAGCACTATGGCTGAGCTGAGCAACAGGTT	3480	QY
QY	3599	CGCACTGGAAAGCGCGTACGTAGCCAAAGGCAACGAACTTACGCTGAC	3540	Db
Db	2678	C-----TGGCACATGCCATGCTGAGCTATGCTGAGCTGAGCTGAGCTGAGCTGAG	2725	QY
QY	3479	AACAACTCACACAGAAAGCTGATGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3420	Db
Db	2778	GGCCATGATAGCTGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	2837	QY
QY	3419	GGCCATGATAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3360	Db
QY	2726	-CAATTAGCCATATTAGTCAGTGGTTATAGATAATGATAATGAGTATTGTT-----ATT	2777	Db
Db	3479	AACAACTCACACAGAAAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3420	QY
QY	2778	GGCCATGATAGCTGATGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	2837	Db
Db	3359	GGCCATGATAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3300	QY
QY	2838	TATGACCGCATGTTGACATGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	2897	Db
Db	3359	TATGACCGCATGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3300	QY
QY	2898	CATTAGTCATGCCATATGGAGTCTGGGTACATACAGTAAAGGAAATGGCCG	2957	Db
Db	3299	CATTAGTCATGCCATATGGAGTCTGGGTACATACAGTAAAGGAAATGGCCG	3240	QY
QY	2958	CTGGTGCACGCCAACGCCAACGCCAACGCCAACGCCAACGCCAACGCC	3107	Db
Db	3239	CTGGTGCACGCCAACGCCAACGCCAACGCCAACGCCAACGCCAACGCC	3180	QY
QY	3018	TAACCCATAGGGACTTCCATTGACGTCATGGTGGAGTATTACGTTAACCTGCC	3077	Db
Db	3179	TAACCCATAGGGACTTCCATTGACGTCATGGTGGAGTATTACGTTAACCTGCC	3120	QY
QY	3078	ACTGGCAGACATCACTGATCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3137	Db
Db	3119	ACTGGCAGACATCACTGATCTGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3060	QY
QY	3138	TAATGCGCCCTGGCATATGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3197	Db
Db	3059	TAATGCGCCCTGGCATATGAGCTGAGCTGAGCTGAGCTGAGCTGAG	3000	QY

Db 2999 AGACATCTAGTATACCTACATCCATGAGATGGCTTGGAGTACATCA 2940
 Qy 3258 ATGGCGCTGAGATGGGTTGACTCACCGGATTCAGTCACCCCATGAGCA 3317
 Db 2939 ATGGCGCTGAGATGGGTTGACTCACCGGATTCAGTCACCCCATGAGCA 2880
 Qy 3318 ATGGAGTTGTTGGCACAAATCAACGGACTTCAAATGCTATAACCG 3377
 Db 2879 ATGGAGTTGTTGGCACAAATCAACGGACTTCAAATGCTATAACCG 2820
 Qy 3378 CCCGTTGAGCAATGGGGTAGGGTACGGGGCTATAAGAGGTC 3437
 Db 2819 CCCATGAGCAATGGGGTAGGGTACGGGGCTATAAGAGGTC 2760
 Qy 3438 GTTTAGTGAGCCGAGATGGGGTAGGGTACGGGGCTATAAGAGGTC 3497
 Db 2759 GTTTAGTGAGCCGAGATGGGGTAGGGTACGGGGCTATAAGAGGTC 2700
 Qy 3498 GACACGGGACCGATCCAGCTCGGAGCGGAGCTGAGGGCTTGGAGGCTATAAGAGGTC 3557
 Db 2699 GACACGGGACCGATCCAGCTCGGAGCGGAGCTGAGGGCTTGGAGGCTATAAGAGGTC 2640
 Qy 3558 GTGCCAAGAGTAGGAGCTACCGCTATAGACTCTATAGGACACCCCTTGCTCTA 3617
 Db 2639 GTGCCAAGAGTAGGAGCTACCGCTATAGACTCTATAGGACACCCCTTGCTCTA 2580
 Qy 3618 TGCATGCTATACCTTTGCTGGGCTATAGACTCTATAGGACACCCCTTGCTCTA 3677
 Db 2579 TGCATGCTATACCTTTGCTGGGCTATAGACTCTATAGGACACCCCTTGCTCTA 2520
 Qy 3678 GATGGATAGCTTGGGTTAGGACCATTTGACCACTCCCTATG 3737
 Db 2519 GATGGATAGCTTGGGTTAGGACCATTTGACCACTCCCTATG 2460
 Qy 3738 GTGACGATCTCCATACATACATACAGCTCTTGCCACACTCTATG 3797
 Db 2459 GTGACGATCTCCATACATACATACAGCTCTTGCCACACTCTATG 2400
 Qy 3798 GCTATATGCCAACTCTGCTCTAGAGACTGACACGGACTCTGCTCTTGCCACACTCTATG 3857
 Db 2399 GCTATATGCCAACTCTGCTCTAGAGACTGACACGGACTCTGCTCTTGCCACACTCTATG 2340
 Qy 3858 GGGTCCCAATTATTTACAAATCACATACACGGCTCCCGGCCCCGGAG 3917
 Db 2339 GGGTCCCAATTATTTACAAATCACATACACGGCTCCCGGCCCCGGAG 2280
 Qy 3918 TTTTAAACATAGCTGGGATCTCGGGATCTGGGACTGTTCCGACATGG 3977
 Db 2279 TTTTAAACATAGCTGGGATCTCGGGATCTGGGACTGTTCCGACATGG 2220
 Qy 3978 GCTCTCTCGGGATCGGGAGCTCCACATCGAGCTGGGCTGGTCCCTGAGCTGG 4037
 Db 2219 GCTCTCTCGGGATCGGGAGCTCCACATCGAGCTGGGCTGGTCCCTGAGCTGG 2160
 Qy 4038 CTCTGGCTGGGAGCTCTCTGCTCTAACAGTGAGGCCAGCTTGGACAC 4097
 Db 2159 CTCTGGCTGGGAGCTCTCTGCTCTAACAGTGAGGCCAGCTTGGACAC 2100
 Qy 4098 ATATCCACACCACTGTCGGCACAGGGCTGGGGTAGGGTGTGCTGAA 4157
 Db 2099 AATGCCAACACCACTGTCGGCACAGGGCTGGGGTAGGGTGTGCTGAA 2040
 Qy 4158 TGAGCTCGGAGATGGGCTGCAACCGCTGAGAGACTTAAGGAGGGAGA 4217
 Db 2039 TGAGCTCGGAGATGGGCTGCAACCGCTGAGAGACTTAAGGAGGGAGA 1980
 Qy 4218 AGAGATGAGGAGGAGCTGAGTGTGTTGATAAGAGTCAAGGAAATCCCGTGC 4277
 Db 1979 AGAGATGAGGAGGAGCTGAGTGTGTTGATAAGAGTCAAGGAAATCCCGTGC 1920
 Qy 4278 GGCTCTGTTACGGGAGGAGCTGAGTGTGTTGAGGAGTCTGAGCTGTC 4337

Db 1119 GTGTGCTTAAAGGTGGAGGAGCTGAGTGTGAGGAGTCTGTCCTCGGAGCGGC 1860
 Qy 4338 CACCAAGCATATAAGCTGAGCAGACTACAGACTGTCCTTCATGGTCCTTCTGAG 4397
 Db 1859 CACCAAGCATATAAGCTGAGCAGACTACAGACTGTCCTTCATGGTCCTTCTGAG 1800
 RESULT 4
 ADD3560/c
 ID ADD3560 standard; DNA; 7086 BP.
 XX
 AC ADD3560;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 Tricistronic eukaryotic expression vector pL249.
 XX
 Multicistronic eukaryotic expression vector; multiple protein expression;
 KW simultaneous expression; viral internal ribosomal entry site; viral IRES;
 KW chain terminator; transcription pause site; gene transfer;
 DNA immunization; gene therapy; PL90; Kanamycin resistance gene;
 KW cytomegalovirus; CMV promoter/enhancer; CMV intron A;
 encephalomyocarditis virus; EMCV IRES; SV40 polyadenylation site;
 KW Rous sarcoma virus; RSV promoter; rabbit betaglobin intron;
 mRGA terminator; cyclic; circular; ds.
 XX
 OS Chimeric.
 OS Synthetic.
 OS Human herpesvirus 5.
 OS Encephalomyocarditis virus.
 OS Simian virus 40.
 OS Rous sarcoma virus.
 OS Oryctolagus cuniculus.
 OS Escherichia coli.
 XX
 PN WO2003031630-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 10-OCT-2002; 2002WO-IT000646.
 XX
 PR 12-OCT-2001; 2001IT-MI002110.
 XX
 PA (KERY-) KERYOS SPA.
 XX
 PI Fazio V, Rinaldi M, Sonzogni L, Tonon G, Orsini G;
 XX
 DR WPI; 2003-39344/37.
 XX
 PT New multicistronic recombinant plasmid vectors expressing two to our
 genes simultaneously, useful in various biotechnological applications,
 such as gene transfer, gene therapy and in DNA immunization.
 XX
 PS Claim 18; SEQ ID NO 3; 52pp; English.
 XX
 The invention relates to multicistronic eukaryotic expression vectors for
 the expression of at least two proteins of interest which may be
 identical or different. The vectors comprise at least one eukaryotic
 expression cassette having a promoter/enhancer sequence, an intron
 sequence, a cloning site, a viral internal ribosomal entry site (IRES)
 and a chain terminator. The vectors may additionally contain a
 transcription pause site downstream of the chain terminator. The
 invention also encompasses eukaryotic host cells comprising a vector of
 the invention, and the recombinant expression of two or more eukaryotic
 proteins using host cells transformed with a vector of the invention.
 The vectors are useful in various biotechnological applications in which
 the simultaneous expression of two or more genes is necessary, such as
 gene transfer protocols, DNA immunisation, or for the expression of
 different molecules in the same cell. They may also be used in gene
 therapy. The present sequence represents a specifically claimed vector
 designated pL249, which comprises a cytomegalovirus (CMV)
 promoter/enhancer, CMV intron A, the encephalomyocarditis virus (EMCV)
 IRES, an SV40 polyadenylation site, a transcription pause site, a Rous

Db	2087	GGCAGTGGAGGCAACGCAATAATGAGTAGCTACTCATAGGACCCAGCTT	Db	3165	TAATGGATAGETTAGCTAGGTTGGGTATGACCAATTATGACCAACTCCCTATT
Qy	2658	CCGATAGGGGACATCAAGCTGCACTGGCRATGATATGATCTATATGATC	Qy	3737	G37GACGAACTTCCATTAACTATCCATAACATGGCTTGGCCAAACATCTGATT
Db	2147	ACACTTATGCTTGGCTGGTGTGTTGTTGGAGGATACATTACAC	Db	3225	GGTACCAACTTCCATTAACTATGCTTGGCCAAACATCTGATT
Qy	2718	AATATGGCAATTAGCCATTAGTCATGGTATATAGCAATAATCATATTGGCTT	Qy	3797	G37GATATGCCAACTACTCTGCTTGGAGACTGACAGGACTCTTATTGAGGAT
Db	2207	AGGAACAGCTATGACCAATGATTAGCCAGCTAGTCGAATAATCATATTGGCTT	Db	3285	GGTATAGCCAACTACTCTGCTTGGAGACTGACAGGACTCTTATTGAGGAT
Qy	2778	GGCATTGCAATGCTGTTATCTATATCAATAATGACATTATGGCTATGTCAA	Qy	3857	G37GTCATTATTAACAAATACATACACAAAGCCGCCCCGTGCGGCA
Db	2257	GGCATTGCAATGCTGTTATCTATATCAATAATGACATTATGGCTATGTCAA	Db	3345	G37GTCATTATTAACAAATACATACACAAAGCCGCCCCGTGCGGCA
Qy	2838	TATACCCCATGTTGACATGTGTTATCTATATCAATAATGACATTATGGCTATGTCAA	Qy	3917	GTTTTATTAACATAGCGTGGATCTCAGGAAATCTGGTCCAGGATG
Db	2327	TATGACCGCCTATGTTGACATGTGTTATCTATATCAATAATGACATTATGGCTATGTCAA	Db	3405	GTTTTATTAACATAGCGTGGATCTCAGGAAATCTGGTCCAGGATG
Qy	2898	CATTTAGTCATACCCATAATGAGTTGGCTACATACTACGTTAATGGCCG	Qy	3977	G37CTCTTCCGGTAGGGGCGAGCTTCCACATCCGGCCCTGGCTGCGCA
Db	2387	CATTAGTCATAGCCCATATAATGGAGTTGGCTTACATACTTACGGTAATGGCCG	Db	3465	GGCTCTTCCGGTAGGGGCGCTTCCACATCCGGCCCTGGCTGCGCA
Qy	2958	CTGGCTGACGCCAACGCCGCCCTTGACTGATGATGAGCTGTTCCATAG	Qy	4037	GCTCATGTTGCTGGAGCTGCTTCTGCTGCTGAGGTTGGCCAGAC
Db	2447	CTGG-TGACGCCAACGCCGCCATGAGCTGCTAATAGCGTATGTTCCATAG	Db	3525	GCTCATGTTGCTGGAGCTGCTTCTGCTGCTGAGGTTGGCCAGAC
Qy	3018	TAAGCCAAATGGGAACTTTCATGACGTCATGGTGAATTACGGTAACTGCC	Qy	4097	CAATGCCACCCACGCTGAGCTGCTTCTGCTGAGGTTGGCCAGAC
Db	2506	TAAGCCAAATGGGAACTTTCATGACGTCATGGTGAATTACGGTAACTGCC	Db	3585	CAATGCCACCCACGCTGAGCTGCTTCTGCTGAGGTTGGCCAGAC
Qy	3078	ACTTGGCAGTACATCAAGTGTATCATATGCCAACTCC-GCCCTATTGACGTCATGAC	Qy	4157	ATAGCTGGAGATGGCTGACCCCTGAGCTGAGGAGACTTAAGGAGCG
Db	2566	ACTTGGCAGTACATCAAGTGTATCATATGCCAACTCC-GCCCTATTGACGTCATGAC	Db	3645	ATAGCTGGAGATGGCTGACCCCTGAGCTGAGGAGACTTAAGGAGCG
Qy	3137	GTAATATGCCCGCTGGCTTATGCCGACTGTGACCTACGGACTTCTACTGG	Qy	4217	AGACAGATGCAAGCAGTGAGTTGTGTTATCTGATAGAGTCAGGTAACTCCGGTG
Db	2626	GTTTAATGGCCCGCTGGCTTATGCCGACTGTGACCTACGGACTTCTACTGG	Db	3704	AGAAGAGCAGCAGCTGAGTTGTGTTATCTGATAGAGTCAGGTAACTCCGGTG
Qy	3197	CAGTACATCTAGTATTACTCATGCTTATACATGGTGTGCTGGTTTGCGAGTACACC	Qy	4277	CGGTGCTTAACTGGTGGAGGAGTGTGAGGAGTCTGTTGCTGGCGGGCG
Db	2686	CAGTACATCTAGTATTACTCATGCTTATACATGGTGTGCTGGTTTGCGAGTACACC	Db	3764	CGGTGCTTAACTGGTGGAGGAGTGTGAGGAGTCTGTTGCTGGCGGGCG
Qy	3257	AATGGGGTGTGATAGCGTTTGACTCACGGGATTTCAGTCACCCATGACCT	Qy	4337	CCACCAACATATACTGAGCAGACTACAGACTGTTGGCTTCACTGGCTTTCGCA
Db	2746	AATGGGGTGTGATAGCGTTTGACTCACGGGATTTCAGTCACCCATGACCT	Db	3824	CCACCAACATATACTGAGCAGACTACAGACTGTTGGCTTTCGCA
Qy	3317	AATGGGAACTTGTGTCACGGAAATACGGCACTTCCAAATGCGTAATAACCC	Qy	4397	GTACCCGTCAGCGT
Db	2806	AATGGGAACTTGTGTCACGGAAATACGGCACTTCCAAATGCGTAATAACCC	Db	3884	GTACCCGTCAGCGT
Qy	3377	GCCCCGGTGAACGAAATGGGGTAGGGCTGAGGGAGGCTTATAGCAGACCT	RESULT 7		
Db	2866	GCCCCGGTGAACGAAATGGGGTAGGGCTGAGGGAGGCTTATAGCAGACCT	ID	AB259290	
Qy	3437	CGTTAGTCACCTCAGATCGCTGGAGACGGCATCCAGCTGGCTTGTGACCTCAGA	XX	AB259290;	
Db	2926	CGTTAGTCACCTCAGATCGCTGGAGACGGCATCCAGCTGGCTTGTGACCTCAGA	XX	10-MAY-2003 (first entry)	
Qy	3497	AGACACCGGACCATCCGGCTTGGCGGCCGGAAACGGTGTGACCTGAGGAGATCC	XX	DB	plasmid pPUT2005 SEQ ID NO 5.
Db	2986	AGACACCGGACCATCCGGCTTGGCGGCCGGAAACGGTGTGACCTGAGGAGATCC	XX		ADP-ribosylating exotoxin; immune response; immunisation; vaccine; hCMV; adjuvant; labile enterotoxin subunit B; LTB; human cytomegalovirus; hCMV; human tissue plasminogen activator; circular; cyclic; ds.
Qy	3557	CGTCCAAAGGTGAGTAAAGTACGGCTTATAGCTTATAGGAACCCCTGGCTT	XX		Synthetic.
Db	3046	CGTCCAAAGGTGAGTAAAGTACGGCTTATAGGAACCCCTGGCTT	OS		
Qy	3617	ATGGATGCTTAACTGTGTTGGCTTGGAGGCTTACACCCCCG-TCCATTGCTT	XX		W02003004055-A2.
Db	3106	ATGGATGCTTAACTGTGTTGGCTTGGAGGCTTACACCCCCG-TCCATTGCTT	XX		16-JAN-2003.
Qy	3677	TGTTGTTAGCTTAGCTTATAGCTGTCGGTTATGACATTATGACCACTCCCTT	XX		26-NOV-2001; 2001WO-US043151.

Qy	3197	CACTAATCTAGTATAGTCATCGCTTATTACCATGGGATGGGTTGGGACTACCC	3256
Db	2686	CAGTACATCTAGTATAGTCATCGCTTATTACCATGGGATGGGTTGGGACTACCC	2745
Qy	3257	AATGGCGGTGGATAGCGGTTGACTCAGGGGATTCCAGTCACCCATTGAGTC	3316
Db	2746	AATGGCGGTGGATAGCGGTTGACTCAGGGGATTCCAGTCACCCATTGAGTC	2805
Qy	3317	AATGGCGGTGGATAGCGGTTGACTCAGGGGATTCCAGTCACCCATTGAGTC	3376
Db	2806	AATGGCGGTGGATAGCGGTTGACTCAGGGGATTCCAGTCACCCATTGAGTC	2865
Qy	3377	GCCCCGTTGACCCAAATGGGCGTAGGGCTGAGCTGGGGCTTATAGCAGAGCT	3436
Db	2866	GCCCCGTTGACCCAAATGGGCGTAGGGCTGAGCTGGGGCTTATAGCAGAGCT	2925
Qy	3437	CGTTTACTGACACGGTCAAGTCGCTGAGTCAGCGCTGGAGACGGCATTCAC	3496
Db	2926	CGTTTACTGACACGGTCAAGTCGCTGAGTCAGCGCTGGAGACGGCATTCAC	2985
Qy	3497	AGACACGGGACCGATTCAGCGCTGGAGACGGCATTCACCGCTGTTGACCT	3556
Db	2986	AGACACGGGACCGATTCAGCGCTGGAGACGGCATTCACCGCTGTTGACCT	3045
Qy	3557	CCTGCCAAAGACTGACCTAAGTACCGCTATAGCTTATAGSCACCCCTTGGCTT	3616
Db	3046	CCTGCCAAAGACTGACCTAAGTACCGCTATAGCTTATAGSCACCCCTTGGCTT	3105
Qy	3617	ATGCCATGCTACTGTTTGGCTGGGCTTAAACCCCCCTCTTATAGCTT	3676
Db	3106	ATGCCATGCTACTGTTTGGCTGGGCTTAAACCCCCCTCTTATAGCTT	3164
Qy	3677	TGATGTTAGCTATAGCTTGTGTTGGGTAACTAGGTGGGTTATGACCACT	3736
Db	3165	TGATGTTAGCTATAGCTTGTGTTGGGTAACTAGGTGGGTTATGACCACT	3224
Qy	3737	GCTGACCACTACTTCCTAACTAATGCCATGCTTTCACACTATCTT	3796
Db	3225	GCTGACCACTACTTCCTAACTAATGCCATGCTTTCACACTATCTT	3284
Qy	3797	GGCTATATGCCAACTACTGTCTTCAAGACTCAACGGACTCTGTTTACAGAT	3856
Db	3285	GGCTATATGCCAACTACTGTCTTCAAGACTCAACGGACTCTGTTTACAGAT	3344
Qy	3857	GGGGTCCCATTATTATTTACAATTCACATACAAACAGCGCTCCCCGGCCCCA	3916
Db	3345	GGGGTCCCATTATTATTTACAATTCACATACAAACAGCGCTCCCCGGCCCCA	3404
Qy	3917	GTTTTATAACATACCGTGGATCTCACCGAATCTCGGCTAAGCTTCCGACATG	3976
Db	3405	GTTTTATAACATACCGTGGATCTCACCGGGAATCTCGGCTAAGCTTCCGACATG	3464
Qy	3977	GGCTCTTCTCCGGTAGCGCGGGAGCTTCCACATCCAGGCCCTGGTCCATGCCCTCAGCG	4036
Db	3465	GGCTCTTCTCCGGTAGCGCGGGAGCTTCCACATCCAGGCCCTGGTCCATGCCCTCAGCG	3524
Qy	4037	GCTCTATGGCTGGCGAGCTCTTGTCTCTAACATGTTGGAGGCGAAGCTTACCAACCA	4096
Db	3525	GCTCTATGGCTGGCGAGCTCTTGTCTCTAACATGTTGGAGGCGAAGCTTACCAACCA	3584
Qy	4097	CAATGCCACCAACCGTGGCCACAAAGCCCTGGGGTAGGGATGCTCGAA	4156
Db	3585	CAATGCCACCAACCGTGGCCACAAAGCCCTGGGGTAGGGATGCTCGAA	3644
Qy	4157	ATGAGCTGGAGATTGGAGCTGGCTCGACCGTGAGCTGGAGACTTAAAGCGGGAG	4216
Db	3645	ATGAGCTGGAGATTGGAGCTGGCTCGACCGTGAGCTGGAGACTTAAAGCGGGAG	3703
Qy	4217	AAGAGAATGCAAGGCGAGCTGGCTCGACCGTGAGCTGGAGACTTAAAGCGGGAG	4276
Db	3704	AAGAGAATGCAAGGCGAGCTGGCTCGACCGTGAGCTGGAGACTTAAAGCGGGAG	3763

4277 CGGTCGTGTTAACGGTGGAGGGCAGTGACTCTGAGCAGTACTCGTGTGCTCCGGCGCG 4336
 3764 CGGTGCTGTTAACGGTGGAGGGCAGTGACTCTGAGCAGTACTCGTGTGCTCCGGCGCG 3823
 4337 CCACAGAGATAATAGCTGAGCAGACTAACGACTCTGTCCTTCATGGGCTTTCATGCA 4396
 3824 CCACAGAGATAATAGCTGAGCAGACTAACGACTCTGTCCTTCATGGGCTTTCATGCA 3883
 4397 GTCACCGTCCACCGCT 4412
 3884 GTCACCGTCCACCGCT 3899

LT 8
 9291
 AB259291 standard; DNA; 5488 BP.

AB259291;

10-MAY-2003 (first entry)

Plasmid pPJ2006 SEQ ID NO 6.

ADP-ribosylating exotoxin; immune response; immunisation; vaccine; adjuvant; labile enterotoxin subunit A; LTA; human cytomegalovirus; human tissue plasminogen activator; circular; cyclic; ds. Synthetic.

WO2003004055-A2.

16-JAN-2003.

26-NOV-2001; 2001WO-US043151.

27-NOV-2000; 2000US-00724315.

(POWD-) POWDERJECT VACCINES INC.

Haynes JR, Arrington JE;

WPI: 2003-221541/21.

New compositions comprising nucleic acid adjuvants, useful in immunization techniques, particularly for eliciting or enhancing an immune response against an antigen in a human.

Example 2; Fig 6; 143pp; English.

The invention relates to a composition comprising: (a) a first nucleic acid sequence that is a truncated A subunit coding region obtained or derived from a bacterial ADP-ribosylating exotoxin; and (b) a second nucleic acid sequence that is a truncated B subunit coding region obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of the truncated subunit coding regions has a 5' deletion and encodes a subunit peptide not having an amino terminal bacterial signal peptide. The composition is useful for eliciting an immune response against an antigen or for manufacturing a medicament for enhancing an immune response in a vertebrate subject (specifically a human) against an antigen. The composition is particularly useful as nucleic acid adjuvants for use in immunisation techniques. The present sequence is that of a plasmid expression vector that contains a truncated coding sequence for an *E. coli* heat labile enterotoxin (LT) subunit A (LTA) peptide with a deletion of the C-terminal RDR motif, the human cytomegalovirus (HCMV) immediate early promoter and associated intron A sequence and the coding sequence for the signal peptide of human tissue plasminogen activator, to allow for secretion from mammalian cells of the truncated LTA expression product.

PI Haynes JR., Arrington JE;

XX WPI: 2003-221541/21.

DR

XX

PT

XX

New compositions comprising nucleic acid adjuvants, useful in immunization techniques, particularly for eliciting or enhancing an immune response against an antigen in a human.

PS

XX Example 1: Fig 1; 143pp; English.

The invention relates to a composition comprising: (a) a first nucleic acid sequence that is a truncated A subunit coding region obtained or derived from a bacterial ADP-ribosylating exotoxin; and (b) a second nucleic acid sequence that is a truncated B subunit coding region obtained or derived from a bacterial ADP-ribosylating exotoxin. Each of the truncated subunit coding regions has a 5' deletion and encodes a subunit peptide not having an amino terminal bacterial signal peptide. The composition is useful for eliciting an immune response or for manufacturing a medicament for enhancing an immune response in a vertebrate subject (specifically a human) against an antigen. The composition is particularly useful as nucleic acid adjuvants for use in immunisation techniques. The present sequence is that of a plasmid expression vector that contains a truncated coding sequence for a cholera toxin (CT) subunit A (CTA) peptide, the human cyromegalovirus (HCMV) immediate early promoter and associated intron A sequence and the coding sequence for the signal peptide of human tissue plasminogen activator, to allow for secretion from mammalian cells of the truncated CTA expression product.

CC Sequence 5500 BP; 1373 A; 1336 C; 1373 G; 1418 T; 0 U; 0 Other;

CC Query Match 37.1%; Score 2378.8; DB 7; Length 5500;

CC Best Local Similarity 31.6%; Pred. No. 0; Mismatches 197; Indels 41; Gaps 6;

CC

QY

DB

QY

Db	1607	ATACCTACAGCTGAGGAATGGAAGAGGCCAGCTTCCGAGGGAGAAAGGCCAG	1666
Db	2215	GTATCCGTAACGGCGGGGCGGAACAGGAGACGCCACGAGGGAA	2274
Db	1667	GTATCCGTAACGGCGGGGCGGAACAGGAGACGCCACGAGGGAA	1726
Db	2275	CGCTCTGATCTTATAGTCMGTGCGAGCTCTGAGCTCGATTT	2334
Db	1727	CGCTCTGATCTTATAGTCMGTGCGAGCTCGATTT	1786
Db	2335	GTATCTGCGAGGGGGCGAGCTATGGAAAAGGCCGCAAGCCGCTT	2394
Db	1787	GTATCTGCGAGGGGGCGAGCTATGGAAAAGGCCGCAAGCCGCTT	1846
Db	2395	GTCTCTGCCTTGTGCGGCTTGTGAGCTGCTGCGTATCCCTGATC	2454
Db	1847	GTCTCTGCCTTGTGCGGCTTGTGAGCTGCTGCGTATCCCTGATC	1906
Db	2455	TGTTGATACCCATTACCGCGATGCTATTGATTAATGATC-----ATT	2505
Db	1907	TGTTGATACCCATTACCGCGATGCTATTGATTAATGATC-----ATT	1966
Db	2506	CGGGTTATTAGTCATAGCCATATTTGAGCTTCCGTTACATAACTACGGTAAT	2565
Db	1967	CGGGCTGTCGTCGACCCCGAACGACCCGCCATTGACGCTAATAGGAG-----	2026
Db	266	GCCGCTGTCGTCGACCCCGAACGACCCGCCATTGACGCTAATAGGAG-----	2620
Db	2027	CCCCGGCGTGGCGATTCAATATCAGCTGGACAGGTTCCGACTGGAAAGC	2086
Db	2621	-----ATCTGATATAGGAGACAGCAGATACTGGCTATATCG	2657
Db	2087	GGGCAGTGAGCGCAACCGAATTATGCTGAGTTAGCTACTCATAGGACCCAGCTT	2146
Db	2658	CGGATAGGGCACATCAAGCTGGCACATGGCAACGATCATGATCATGATC	2717
Db	2147	ACACTTATGCTCCGCTCGTAGTGTGTGAGTGTGAGGGATAACATTGCA	2206
Db	2718	AATATTGCAATTAGCCTATTAGTCATGTTATAGCTAAATCATATTGCTT	2777
Db	2207	AGGAACGCTATGACCATGATACGCCAACTGAGCTACGACAATAATCATATTGCTT	2266
Db	2778	GSCCATGTCATGTTGATATGTCATATGTCATATTGTCATGTC	2837
Db	2267	GGCCATTCATAGTTGATATGTCATATGTCATGTC	2326
Db	2838	TATGACGCCATGTTGACATGTTGACTGTTGAGTTATAGTAAATCAATTACGGGT	2897
Db	2327	TATGACGCCATGTTGACATGTTGACTGTTGAGTTATAGTAAATCAATTACGGGT	2386
Db	2898	CATTAGTCATGCCATATGGAGTTCGGTTAGATAACTTACGTAATTGGCA	2957
Db	2387	CATTAGTCATGCCATATGGAGTTCGGTTAGATAACTTACGTAATTGGCA	2446
Db	2958	CTGGCTTACGCCAACGACCCCGCCATTCAGCTAATGAGCTATGTC	3017
Db	2447	CTCG-TAACGCCAACGACCCCGCCATTCAGCTAATGAGCTATGTC	2505
Db	3018	TAACGCCAATGGACTTCATGGAGCTAATGGGGGATTTGGTAACGCC	3077
Db	2506	TAACGCCAATGGACTTCATGGAGCTAATGGGGGATTTGGTAACGCC	2565
Db	3078	ACTGGAGTACATCAAGTGTACATGCGAAGTCGCCCTATGCGTAATGAC	3136
Db	2566	ACTGGAGTACATCAAGTGTACATGCGAAGTCGCCCTATGCGTAATGAC	2625
Db	3137	GTAATAGGCCCTGCTGAGCTATGCGAAGTCGCCCTATGCGTAATGAC	3196
Db	2626	GTTAAATGCCGCTGCTGAGCTATGCGAAGTCGCCCTATGCGTAATGAC	2685
Db	3197	CAGTACATCTAATGTCATGCGTATTACCATGCGTTTGCGAGTAC	3256
Db	2686	CAGTACATCTAATGTCATGCGTATTACCATGCGTTTGCGAGTAC	2745

Y	3317	AATGGGGTGTGTTGGGACCAATTCAGGGACTTCAAGTCTCCGCCCATGGTC	3316	4337	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	4396
b	2746	AATGGGGTGTGATAGCGGTTGACTACGGGATTTCAGGGATTTCAGCT	2805	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3317	AATGGGGTGTGTTGGGACCAATTCAGGGACTTCAAGTCTCCGCCCATGGTC	3316	4397	GTACCGTCACGGT	4412
b	2806	AATGGGGTGTGTTGGGACCAATTCAGGGACTTCAAGTCTCCGCCCATGGTC	2805	3884	GTACCGTCACAGCTT	3899
b	3317	GCCCCGTTGACCCAATTCGGCGTAGGGAGGTTCAAGTCTCCGCCCATGGTC	3316	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	2866	GCCCCGTTGACCCAATTCGGCGTAGGGAGGTTCAAGTCTCCGCCCATGGTC	2805	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3437	CGTTTACGTGACCGTCAAGTCCCTGGAGACSCATCACGCTGTTGACCTTCATAGA	3496	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	2926	CGTTTACGTGACCGTCAAGTCCCTGGAGACSCATCACGCTGTTGACCTTCATAGA	2985	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3497	AGACACCGGACCGATTCAGCTCGGGGAGCGTCACTGGGAGGTTCTCCAAATG	3556	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	2986	AGACACCGGACCGATTCAGCTCGGGGAGCGTCACTGGGAGGTTCTCCAAATG	3045	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3557	CCTGCCAGAGTGACGTAGCTTACGGCTATAGCTCTAG3'CAACCCCTTGGCTT	3616	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3046	CCTGCCAGAGTGACGTAGCTTACGGCTATAGCTCTAG3'CAACCCCTTGGCTT	3105	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3617	ATGCATCTATACGTGTTGGCTGGGCTTACACCCCCGTTCTTATGCTATAGG	3676	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3106	ATGCATCTATACGTGTTGGCTGGGCTTACACCCCCGTTCTTATGCTATAGG	3164	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3677	TGATGGTATAGCTTAGCCTATAGGTGTTGGGTTATGACCATTAATGACCACTCCATT	3736	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3165	TGATGGTATAGCTTAGCCTATAGGTGTTGGGTTATGACCATTAATGACCACTCCATT	3224	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3737	GCTGACCATACTTCCTTACATACATCCATAACATGGCTTGCACACTACTCTT	3796	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3225	GGTGACCACTACTTCCTTACATACATCCATAACATGGCTTGCACACTACTCTT	3284	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3797	GCTATATGCCAACTACTCTGCTCTCAGACTGACCGACTCTGTTTTACGGAT	3856	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3285	GCTATATGCCAACTACTCTGCTCTCAGACTGACCGACTCTGTTTTACGGAT	3344	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3345	GGGTCCCATTTATTTACAAATTACATACACACAGCAGCCGCCCC	3916	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3345	GGGTCCCATTTATTTACAAATTACATACACACAGCAGCCGCCCC	3404	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3917	GTTTTATAACATACGGGGATCTCCACGGGATCTCGGTACGTTCCGGACATG	3976	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3405	GTTTTATAACATACGGGGATCTCGGTACGTTCCGGACATG	3464	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3977	GCTCTTCTCCGGTAGGGGGCTTCAACTCGGGCTTCCTGGCTCCACCG	4036	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3465	GCTCTTCTCCGGTAGGGGGCTTCAACTCGGGCTTCCTGGCTCCACCG	3524	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	4037	GTCATCTGCTGGGGCTCTCTAACAGTGAGGGAGCTTCAACCTGGCTCCAC	4096	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3525	GTCATCTGCTGGGGCTCTCTAACAGTGAGGGAGCTTCAACCTGGCTCCAC	3584	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	4097	CAATGCCAACACCAACAGTGGCGCAAGGGCGTGGGTTAGGGATGTCGAA	4156	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3585	CAATGCCAACACCAACAGTGGCGCAAGGGCGTGGGTTAGGGATGTCGAA	3644	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	4157	ATGAGCTGGAGATGGCTCACCCTGACCGAGCTTAAGGAGCGCG	4216	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3645	ATGAGCTGGAGATGGCTCACCCTGACCGAGCTTAAGGAGCGCG	3703	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	4217	AGAGAGTGACCGAGCTGAGGTGTTGATTCAGTCAAGTCAAGTCAAGT	4276	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3704	AGAGAGTGACCGAGCTGAGGTGTTGATTCAGTCAAGTCAAGTCAAGT	3763	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	4277	CGGTGCTTAAAGGGAGGGAGGTGAGTCTGAGCACTACTGTGTG	4336	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883
b	3764	CGGTGCTTAAAGGGAGGGAGGTGAGTCTGAGCACTACTGTGTG	3823	3824	CCACCAAGACTAATAGCTGACAGACTACAGACAGTCAGTCCTTCTGCA	3883

The present invention relates to a composition comprising a first vector with a vaccine insert encoding one or more antigens that elicit an immune response against HIV or a first subtype or recombinant form; and a second vector comprising a vaccine insert encoding one or more antigens that elicit an immune response against an HIV of a second subtype or recombinant form. The composition is useful in generating an immune response against HIV. The insert of the first vector or the insert of the second vector comprises the sequences of two or more of: a gag, pol, env, rev, nef, vit, vpr or vpu gene; or their mutants; and optionally, non-coding regulatory sequences of the HIV genome. At least one of the two or more sequences comprises mutations that limit the encapsidation of viral RNA, or a gag sequence having a mutation in one or more of the sequences encoding a zinc finger. All or part of cis-acting RNA encapsidation sequences have been deleted from the non-coding regulatory sequences of HIV-1. The two or more sequences comprise a pol sequence having a mutation that inhibits one or more of the enzymatic activities of pol. The enzymatic activity is integrase activity, reverse transcriptase activity or protease activity. The enzymatic activity is inhibited by deleting a portion of the pol sequence or introducing one or more point mutations into the pol sequence. The present sequence is one such vector used to illustrate the invention.

XX
SQ Sequence 10466 BP; 3317 A; 2200 C; 2543 G; 2405 T; 0 U; 1 Other;

Query Match 31.6%; Score 2027.6; DB 9; Length 10466;
 Best Local Similarity 87.4%; Pred. No. 0;
 Matches 2407; Conservative 1; Mismatches 15; Indels 331; Gaps 4; B

Db
8101 AATCCCTTAACGTGAGTTTCGTTCCACTGAGCGTCAGACCCGTAGAAAGATCAAGG 8166

1774 ATCTTCTTGTAGATCTTTTTCTGCGCGTAACTGCTGCTTGCAAAACAAAAACCC 18333
Oy

Db	8161 ATCTCTGAGATCCCTTTTCTGGCGTAACTGCGCTTGGAAACAAAAACCC
Qv	1834 GCTTACCCAGCTGTGTTTGGATCAGAGCTTCAAATTTTCTTCAAGCTAC 1893

Db	Accession	Sequence	Length
8221	GCTAACGCGGTGGTTGTTGGGGATCAAGACTTACCAACTCTTTCCGAAGGTAC	8286	1625

1894 TGGCTTCAGCAGAGGCAGATAACCAAATACGTCTCTCTAGTGTAGCCGTAGTTAGGCCA 1953

Db 8281 TGGCTTCAGCAGAGCGCAGATACTCAAATCTGTTCTCTAGTGTAGCCGTAGTTAGGCCA 8341

Qy	Dp	1954	2011
	8341	CCATTCAAGAACCTGTAGCCACGCCCTACATAACCTCGCTGCTAACTCTGTACAGT	8400

QY 2014 GGCCTGCGCAGTGGATAAATGCTGCTTACGGGTTGACTCAAGCGATAGTTC 2073

8401 GCCTGCTGCCAGGGCAATAGCTGTCTTACCGGGTTGGACTCAAGACCAATAGTTAC 8466
Db

8Y	2134	AACGGACCTACACCCGAACTGAGATACCTACAGGGTGTAGCTATGAGAAAGGCCACGCTTCC	2193
DB	8461	GGATTAAGGAGGAGGGTGTAGAAGGGGAGTCTGAGACAGACAGCCACGCTGGAGCG	8520

8521 AACGACCTACACGGAACTGAGATACCTACAGGTGAGCTATGAGAAAGGCCACGCTCC 85866

QY
2194 CGAAGGGAGAAAGGGGACAGGTTATCCGGTAAGGGCAGGGTCGGAACAGGAGAGCCCCAC 2253

Db 8581 CGAAGGGAGAAAGGGGGACAGGTTACCGTAACGGCAGGGCTGGAAACGGAGAGCCAC 864

QY	2234	GAAGGAGCTTCAAGGGGAAACGGCTGGTAACTTATAGTCCTGGGTTTGGCCACCT	2313
Db	8641	GAGGGAGCTTCAGGGGGAAACCGCTGGTATCTTATAGTCCTGGGTTTGGCCACCT	8700

8Y 2314 CTGACTTGCAGCGTCGATTTCGTGATGCTCGTCAGGGGGCGAGCCTATGGAAAAACGC 2373

Db	QY	3452	CAGNTGGCTGGAGAACGACATCCACCTGTTGACCTCCATAGAGAACCGGGACCGA	3511	Db
Db	Q9513	9513	CAGATCGCTGGAGAACGACATCCACCTGTTGACCTCCATAGAGAACCGGGACCGA	9572	DE
Db	QY	3512	TCCAGGCTCCGG	3571	XX
Db	QY	9573	TCCAGGCTCCGG	9632	XX
Db	QY	3572	GTAACTACCGCCATAGACTCTAGGACACCCCTTGCTCTATGCACTTAACTG	3631	KW
Db	QY	9693	TTTGTGGCTGGGGCTTATACACCCCGCTTCCTATGCTATGGCACTCCGTC	9752	HIV infection; Anti-HIV; vaccine; ds
Db	QY	3692	GCCTATAGCTGGGGTTATGACCATTTATGACCACTGGCTATGGCACTCCGTC	3751	XX
Db	QY	9753	GCCTATAGCTGGGGTTATGACCATTTATGACCACTGGCTATGGCACTCCGTC	9752	Synthetic.
Db	QY	3632	TTTTGGCTGGGGCTTACACCCCGCTTCCTATGCTATAGGTGATGGATAGCTA	3691	XX
Db	QY	9645	TTTGTGGCTGGGGCTTATACACCCCGCTTCCTATGCTATGGCACTCCGTC	9645	XX
Db	QY	3645	GCCTATAGCTGGGGTTATGACCATTTATGACCACTGGCTATGGCACTCCGTC	3751	XX
Db	QY	9692	GTAACTACCGCCATAGACTCTAGGACACCCCTTGCTCTATGCACTTAACTG	9692	XX
Db	QY	3692	GCCTATAGCTGGGGTTATGACCATTTATGACCACTGGCTATGGCACTCCGTC	3751	XX
Db	QY	9753	GCCTATAGCTGGGGTTATGACCATTTATGACCACTGGCTATGGCACTCCGTC	9752	XX
Db	QY	3752	CATTACTATCCATACTAGGCTCTTGCACACTACTCTCTATGGCTATGGCA	3811	XX
Db	QY	9813	CATTACTATCCATACTAGGCTCTTGCACACTACTCTCTATGGCTATGGCA	9872	XX
Db	QY	3812	CCTGTGCTTCAGAGACTCACCGACTCTGTTAACGATTTACAGATGGGCTTCA	3871	XX
Db	QY	9873	CCTGTGCTTCAGAGACTCACCGACTCTGTTAACGATTTACAGATGGGCTTCA	9932	XX
Db	QY	3872	ATTTACAATTCACTATCACACACAGCGCTTCCCGTCCCCAGTTTAACTAT	3931	XX
Db	QY	9933	ATTACANATTCACTATCACACACAGCGCTTCCCGTCCCCAGTTTAACTAT	9992	XX
Db	QY	3932	AGGGTGGATCTCAAGGGAATCTGGGTA-CCTGTCGGACATGGCTCTCTCCGT	3990	XX
Db	QY	9993	AGGGTGGATCTCAAGGGAATCTGGGTA-CCTGTCGGACATGGCTCTCTCCGT	10052	XX
Db	QY	3991	AGCGCGGGAGCTTACACATCCAGGCGCTGGTCCATGCTTCCAGGGCTCATGTC	4050	XX
Db	QY	10053	AGCGCGGGAGCTTACACATCCAGGCGCTGGTCCATGCTTCCAGGGCTCATGTC	10112	XX
Db	QY	4051	GGCGAGCTCTGGCTCTAACAGTGGAGGCGAGACTTACGGACACATGCCACACC	4110	XX
Db	QY	10113	GGCGAGCTCTGGCTCTAACAGTGGAGGCGAGACTTACGGACACATGCCACACC	10172	XX
Db	QY	4111	ACCGATGCGCGAACAGCCGGTGGGGTAGGGTATGGCTCTGAAATGAGCTGGAG	4170	XX
Db	QY	10173	ACCGATGCGCGAACAGCCGGTGGGGTAGGGTATGGCTCTGAAATGAGCTGGAG	10232	XX
Db	QY	4171	TGGCTCGACCGGTGACCCAGATGGAGACTTAAAGGCGGGAAAGAGATGCGGC	4230	XX
Db	QY	10233	TGGCTCGACCGGTGACCCAGATGGAGACTTAAAGGCGGGAAAGAGATGCGGC	10292	XX
Db	QY	4231	AGCTGAGTTGTTGTTCTGAGAGCTTAAAGGCGGGAAAGAGATGCGGC	4290	XX
Db	QY	10293	AGCTGAGTTGTTCTGAGAGCTTAAAGGCGGGAAAGAGATGCGGC	10352	XX
Db	QY	4291	GTGGAGGGAGTGTGTTCTGAGAGCTTAAAGGCGGGAAAGAGATGCGGC	4350	XX
Db	QY	10353	GTGGAGGGAGTGTGTTCTGAGAGCTTAAAGGCGGGAAAGAGATGCGGC	10412	XX
Db	QY	4351	AGCTGAGAGACTAAAGAATGGTCTTCCATGGCTTCTGGAGTACCGT	4404	XX
Db	QY	10413	AGCTGAGAGACTAAAGAATGGTCTTCCATGGCTTCTGGAGTACCGT	10466	XX
RESULT 13					
ADE06466					
ID					
XX					
AC					
XX					

CC having a mutation that inhibits one or more of the enzymatic activities
CC of pol. The enzymatic activity is integrase activity, reverse
CC transcriptase activity or protease activity. The enzymatic activity is
inhibited by deleting a portion of the pol sequence or introducing one or
more point mutations into the pol sequence. The present sequence is one
CC such vector used to illustrate the invention.
CC
XX

8024	ACTGGGTTCTAGGTGAAAGGTTAGCTGACCAA	8083	QY	1714	AATCCCTAACGAGGTTGCGTCAGACCGGAGAAAGTCAAGG	1773	Db
8084	AATCCCTAACGAGGTTGCGTCAGACCGGAGAAAGTCAAGG	8143	Db	8084	AATCCCTAACGAGGTTGCGTCAGACCGGAGAAAGTCAAGG	8143	Db
1774	ATCTTCTGAGATCTTCTTCTGGGGTAATCTGCTCTTGAAACAAACCC	1833	QY	1774	ATCTTCTGAGATCTTCTTCTGGGGTAATCTGCTCTTGAAACAAACCC	1833	Db
8144	ATCTTCTGAGATCTTCTTCTGGGGTAATCTGCTCTTGAAACAAACCC	8203	QY	8144	ATCTTCTGAGATCTTCTTCTGGGGTAATCTGCTCTTGAAACAAACCC	8203	Db
1834	GCTTACAGCGGTGTTTGTGTCGGGATGAAAGGCTTCAACTTTCGAGA	1893	QY	1834	GCTTACAGCGGTGTTTGTGTCGGGATGAAAGGCTTCAACTTTCGAGA	1893	Db
8204	GTCACAGCGGTGTTTGTGTCGGGATGAAAGGCTTCAACTTTCGAGA	8263	QY	8204	GTCACAGCGGTGTTTGTGTCGGGATGAAAGGCTTCAACTTTCGAGA	8263	Db
1894	TGCTCTAGCAGAGGCGATACCAATACTGTTCTCTAGTGCGTAGTTAGGCA	1953	QY	1894	TGCTCTAGCAGAGGCGATACCAATACTGTTCTCTAGTGCGTAGTTAGGCA	1953	Db
8264	TGCTCTAGCAGAGGCGATACCAATACTGTTCTCTAGTGCGTAGTTAGGCA	8323	QY	8264	TGCTCTAGCAGAGGCGATACCAATACTGTTCTCTAGTGCGTAGTTAGGCA	8323	Db
1954	CCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGTAATCTGTTACCGT	2013	QY	1954	CCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGTAATCTGTTACCGT	2013	Db
8324	CCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGTAATCTGTTACCGT	8383	QY	8324	CCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGTAATCTGTTACCGT	8383	Db
2014	GCTCTGCTGCCAGTGGGAATAGTGTGTTACCGGTTGAGAATAGAGGATAGTTAC	2073	QY	2014	GCTCTGCTGCCAGTGGGAATAGTGTGTTACCGGTTGAGAATAGAGGATAGTTAC	2073	Db
8384	GGCTGCTGCCAGTGGGAATAGTGTGTTACCGGTTGAGAATAGAGGATAGTTAC	8443	QY	8384	GGCTGCTGCCAGTGGGAATAGTGTGTTACCGGTTGAGAATAGAGGATAGTTAC	8443	Db
2074	GGATAAGGGAGCGGGTGGGTTGACCGGGGTTGTCACAGCCAGCTGGAGC	2133	QY	2074	GGATAAGGGAGCGGGTGGGTTGACCGGGGTTGTCACAGCCAGCTGGAGC	2133	Db
8444	GGATAAGGGAGCGGGTGGGTTGTCACAGCCAGCTGGAGC	8503	QY	8444	GGATAAGGGAGCGGGTGGGTTGTCACAGCCAGCTGGAGC	8503	Db
2134	AACGAACTAACCGGAACTCGATACTACAGCGGTGAGCTATGAGAAAGGGCACGGTCC	2193	QY	2134	AACGAACTAACCGGAACTCGATACTACAGCGGTGAGCTATGAGAAAGGGCACGGTCC	2193	Db
8504	AACGAACTAACCGGAACTCGATACTACAGCGGTGAGCTATGAGAAAGGGCACGGTCC	8563	QY	8504	AACGAACTAACCGGAACTCGATACTACAGCGGTGAGCTATGAGAAAGGGCACGGTCC	8563	Db
2194	CGAGGGGAAAGGGGAGGGTATCCGTAAGGGAGGGTACGCTGAGGAGGAGGAGC	2253	QY	2194	CGAGGGGAAAGGGGAGGGTATCCGTAAGGGAGGGTACGCTGAGGAGGAGC	2253	Db
8564	CGAGGGGAAAGGGGAGGGTACGCTGAGGAGGAGGAGC	8623	QY	8564	CGAGGGGAAAGGGGAGGGTACGCTGAGGAGGAGGAGC	8623	Db
2254	GAGGGAGCTCCAGGGGAAACGCTGGTATCTTATAGTCTCTGGATTCCACCT	2313	QY	2254	GAGGGAGCTCCAGGGGAAACGCTGGTATCTTATAGTCTCTGGATTCCACCT	2313	Db
8624	GAGGGAGCTCCAGGGGAAACGCTGGTATCTTATAGTCTCTGGATTCCACCT	8683	QY	8624	GAGGGAGCTCCAGGGGAAACGCTGGTATCTTATAGTCTCTGGATTCCACCT	8683	Db
2314	CTGACTTGTAGCGTGTGATTGTGTGATGCTGTCAGGGGGCGGAGCTATGGAAACCC	2373	QY	2314	CTGACTTGTAGCGTGTGATTGTGTGATGCTGTCAGGGGGCGGAGCTATGGAAACCC	2373	Db
8684	CTGACTTGTAGCGTGTGATTGTGTGATGCTGTCAGGGGGCGGAGCTATGGAAACCC	8743	QY	8684	CTGACTTGTAGCGTGTGATTGTGTGATGCTGTCAGGGGGCGGAGCTATGGAAACCC	8743	Db
2374	CAGCAACCGGGCTTTACGGTTCTGGCTTCTGGCTTCTGGCTCATGTTCT	2433	QY	2374	CAGCAACCGGGCTTTACGGTTCTGGCTTCTGGCTTCTGGCTCATGTTCT	2433	Db
8744	CAGCAACCGGGCTTTACGGTTCTGGCTTCTGGCTCATGTTCT	8802	QY	8744	CAGCAACCGGGCTTTACGGTTCTGGCTTCTGGCTCATGTTCT	8802	Db
2434	TCTCTGGTTATCCCCGATCTGTGATACCGTATACGCCATGCTAGTTAA	2493	QY	2434	TCTCTGGTTATCCCCGATCTGTGATACCGTATACGCCATGCTAGTTAA	2493	Db
8803	-----	8802	QY	8803	-----	8802	Db
2494	AGTATCTATTACCGGGTCATTAGCTCATGCCATATGGAGCTCCGGTTACATAC	2553	QY	2494	AGTATCTATTACCGGGTCATTAGCTCATGCCATATGGAGCTCCGGTTACATAC	2553	Db
8803	-----	8802	QY	8803	-----	8802	Db
2554	TTACGGTAATGCCCGCTGGCTACCCCAAGACCCCCGCCATGACGTCATAA	2613	QY	2554	TTACGGTAATGCCCGCTGGCTACCCCAAGACCCCCGCCATGACGTCATAA	2613	Db
8803	-----	8802	QY	8803	-----	8802	Db
2614	TGAGGAGATCTGATATAGGTGACAGACGATATGGCTATATGCCGATAGGGGACAT	2673	QY	2614	TGAGGAGATCTGATATAGGTGACAGACGATATGGCTATATGCCGATAGGGGACAT	2673	Db
8803	-----	8802	QY	8803	-----	8802	Db
2734	CATATAGTCATGGTTATAGCTTAATCAATTGGCTATGGCTCATGCTACGGTAC	2793	QY	2734	CATATAGTCATGGTTATAGCTTAATCAATTGGCTATGGCTCATGCTACGGTAC	2793	Db
8803	-----	8802	QY	8803	-----	8802	Db
2794	GTACTCTATCATATAGTCACTTATAGGTTAGCTCAGTCACTATGCGGATGTC	2853	QY	2794	GTACTCTATCATATAGTCACTTATAGGTTAGCTCAGTCACTATGCGGATGTC	2853	Db
8835	GTACTCTATCATATAGTCACTTATAGGTTAGCTCAGTCACTATGCGGATGTC	8895	QY	8835	GTACTCTATCATATAGTCACTTATAGGTTAGCTCAGTCACTATGCGGATGTC	8895	Db
2854	ACATGTTATGCTAGTGTGTTAGCTGTCAGCTGAGGCTAGACCCGCTAGAAAGTCAAGG	2913	QY	2854	ACATGTTATGCTAGTGTGTTAGCTGTCAGCTGAGGCTAGACCCGCTAGAAAGTCAAGG	2913	Db
8895	ACATGTTATGCTAGTGTGTTAGCTGTCAGCTGAGGCTAGACCCGCTAGAAAGTCAAGG	8955	QY	8895	ACATGTTATGCTAGTGTGTTAGCTGTCAGCTGAGGCTAGACCCGCTAGAAAGTCAAGG	8955	Db
2914	ATATATGGAGTCCGGTTACATRACTACGGTAATGGCCCGCTGGTAGCCCAA	2973	QY	2914	ATATATGGAGTCCGGTTACATRACTACGGTAATGGCCCGCTGGTAGCCCAA	2973	Db
8956	ATATATGGAGTCCGGTTACATRACTACGGTAATGGCCCGCTGGTAGCCCAA	9015	QY	8956	ATATATGGAGTCCGGTTACATRACTACGGTAATGGCCCGCTGGTAGCCCAA	9015	Db
2915	ATATATGGAGTCCGGTTACATRACTACGGTAATGGCCCGCTGGTAGCCCAA	9195	QY	2915	ATATATGGAGTCCGGTTACATRACTACGGTAATGGCCCGCTGGTAGCCCAA	9195	Db
8955	ATATATGGAGTCCGGTTACATRACTACGGTAATGGCCCGCTGGTAGCCCAA	9195	QY	8955	ATATATGGAGTCCGGTTACATRACTACGGTAATGGCCCGCTGGTAGCCCAA	9195	Db
2974	GTACTCTATCATATAGTCACTTATAGGTTAGCTCAGTCACTATGCGGATGTC	3033	QY	2974	GTACTCTATCATATAGTCACTTATAGGTTAGCTCAGTCACTATGCGGATGTC	3033	Db
9016	GTACCCGCCCATGACCTCATATAGGTTAGCTCAGTCACTATGCGGATGTC	9075	QY	9016	GTACCCGCCCATGACCTCATATAGGTTAGCTCAGTCACTATGCGGATGTC	9075	Db
3034	TTTCATTTGACTGTCATGGTTAGCTGCTAGCTGCTAGTTAGGCTAATGGCCCGCTG	3093	QY	3034	TTTCATTTGACTGTCATGGTTAGCTGCTAGCTGCTAGTTAGGCTAATGGCCCGCTG	3093	Db
9076	TTTCATTTGACTGTCATGGTTAGCTGCTAGCTGCTAGTTAGGCTAATGGCCCGCTG	9153	QY	9076	TTTCATTTGACTGTCATGGTTAGCTGCTAGCTGCTAGTTAGGCTAATGGCCCGCTG	9153	Db
3094	AGTGTATCTATGGCCAGTCCGGCCAGGCTTACGGTCAATGGCCCGCTG	3153	QY	3094	AGTGTATCTATGGCCAGTCCGGCCAGGCTTACGGTCAATGGCCCGCTG	3153	Db
9136	AGTGTATCTATGGCCAGGCTTACGGTCAATGGCCCGCTTATGGCTAATGGCCCGCTG	9195	QY	9136	AGTGTATCTATGGCCAGGCTTACGGTCAATGGCCCGCTTATGGCTAATGGCCCGCTG	9195	Db
3154	GCATTATGGCCAGTACAGCTTACGGGACTTCTACTGGCGTACATCTAC-GTAT	3212	QY	3154	GCATTATGGCCAGTACAGCTTACGGGACTTCTACTGGCGTACATCTAC-GTAT	3212	Db
9196	GCATTTAGGCCAGTACAGCTTACGGGACTTCTACTGGCGTACATCTAC-GTAT	9255	QY	9196	GCATTTAGGCCAGTACAGCTTACGGGACTTCTACTGGCGTACATCTAC-GTAT	9255	Db
3213	TAGTCAT-GCTATTACCTGTTGCTGATGCGTTGCGGTTTGGCACTAACCAGGGT	3271	QY	3213	TAGTCAT-GCTATTACCTGTTGCTGATGCGTTGCGGTTTGGCACTAACCAGGGT	3271	Db
9256	TAGTCATCGCTTACCTGCTGATGCGTTGCGGTTTGGCACTAACCAGGGT	9315	QY	9256	TAGTCATCGCTTACCTGCTGATGCGTTGCGGTTTGGCACTAACCAGGGT	9315	Db
3272	GGTTGACTCTACGGGATTCCAGTCTCCACCCCATGACCGCTATGGAGTTGTT	3331	QY	3272	GGTTGACTCTACGGGATTCCAGTCTCCACCCCATGACCGCTATGGAGTTGTT	3331	Db
9316	GGTTGACTCTACGGGATTCCAGTCTCCACCCCATGACCGCTATGGAGTTGTT	9375	QY	9316	GGTTGACTCTACGGGATTCCAGTCTCCACCCCATGACCGCTATGGAGTTGTT	9375	Db
3332	TGGCCACAAATCAACGCGACTTCCAAATGTCGTAATACCGCCCGCTGCGC	3391	QY	3332	TGGCCACAAATCAACGCGACTTCCAAATGTCGTAATACCGCCCGCTGCGC	3391	Db
9376	TGGCACCAAAATCAACGCGACTTCCAAATGTCGTAATACCGCCCGCTGCGC	9435	QY	9376	TGGCACCAAAATCAACGCGACTTCCAAATGTCGTAATACCGCCCGCTGCGC	9435	Db
3392	ATGGGGGTGAGGCTGTTGCTGAGGCTTATAGGAGGCTTCTGAGGAGGCTGTTG	3451	QY	3392	ATGGGGGTGAGGCTGTTGCTGAGGCTTATAGGAGGCTTCTGAGGAGGCTGTTG	3451	Db
9436	ATGGGGGTGAGGCTGTTGCTGAGGCTTATAGGAGGCTTCTGAGGAGGCTGTTG	9495	QY	9436	ATGGGGGTGAGGCTGTTGCTGAGGCTTATAGGAGGCTTCTGAGGAGGCTGTTG	9495	Db
3452	CAGATGCCCTGGAGAGGCCATTCAACGGCTGTTGCTGAGGAGGCTGTTG	3511	QY	3452	CAGATGCCCTGGAGAGGCCATTCAACGGCTGTTGCTGAGGAGGCTGTTG	3511	Db
9496	CAGATGCCCTGGAGAGGCCATTCAACGGCTGTTGCTGAGGAGGCTGTTG	9555	QY	9496	CAGATGCCCTGGAGAGGCCATTCAACGGCTGTTGCTGAGGAGGCTGTTG	9555	Db
3512	TCCAGGCTTCCGGGGCGGAGACGGCTTCAACGGCTGTTGCTGAGGAGGCTGTTG	3571	QY	3512	TCCAGGCTTCCGGGGCGGAGACGGCTTCAACGGCTGTTGCTGAGGAGGCTGTTG	3571	Db
9556	TCCAGGCTTCCGGGGCGGAGACGGCTTCAACGGCTGTTGCTGAGGAGGCTGTTG	9615	QY	9556	TCCAGGCTTCCGGGGCGGAGACGGCTTCAACGGCTGTTGCTGAGGAGGCTGTTG	9615	Db
3572	GTAACTACCCCATAGACTCTATAGGCAACCCCTTGGCTTATGCTGATGCTATAG	3631	QY	3572	GTAACTACCCCATAGACTCTATAGGCAACCCCTTGGCTTATGCTGATGCTATAG	3631	Db
9616	GTAACTACCCCATAGACTCTATAGGCAACCCCTTGGCTTATGCTGATGCTATAG	9675	QY	9616	GTAACTACCCCATAGACTCTATAGGCAACCCCTTGGCTTATGCTGATGCTATAG	9675	Db
3632	TTTGGCTTGGGGCTTACACCCCGCTTCTGCTATGCTGATGCTGATGCTA	3691	QY	3632	TTTGGCTTGGGGCTTACACCCCGCTTCTGCTATGCTGATGCTGATGCTA	3691	Db
9676	TTTGGCTTGGGGCTTACACCCCGCTTCTGCTATGCTGATGCTGATGCTA	9735	QY	9676	TTTGGCTTGGGGCTTACACCCCGCTTCTGCTATGCTGATGCTGATGCTA	9735	Db
3692	GCCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTT	3751	QY	3692	GCCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTT	3751	Db
9736	GCCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTT	9795	QY	9736	GCCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTT	9795	Db
3752	CATTTACCTACATGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTT	3811	QY	3752	CATTTACCTACATGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTT	3811	Db
9796	CATTTACCTACATGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTT	9855	QY	9796	CATTTACCTACATGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTT	9855	Db
3812	CTCTGCTTGGAGACTGACGAGCTGACGAGCTGACGAGCTGACGAGCTGAC	3871	QY	3812	CTCTGCTTGGAGACTGACGAGCTGACGAGCTGACGAGCTGACGAGCTGAC	3871	Db
9856	CTCTGCTTGGAGACTGACGAGCTGACGAGCTGACGAGCTGACGAGCTGAC	9915	QY	9856	CTCTGCTTGGAGACTGACGAGCTGACGAGCTGACGAGCTGACGAGCTGAC	9915	Db

Qy	4111	ACCACTGTCGGCACAAAGCCCTGGGGTGGGGATGTCGCTGAAATGAGCTGGAGAT	4170
Db	10156	ACCACTGTCGGCACAAAGCCCTGGGGTGGGGATGTCGCTGAAATGAGCTGGAGAT	10215
Qy	4171	TGGGCTCGACCGCTGACGGAGATGAGCTAAGGCAAGGGAGAGAGATGGCAGGC	4230
Db	10216	TGGGCTCGACCGCTGACGGAGATGAGCTAAGGCAAGGGAGAGAGATGGCAGGC	10275
Qy	4231	AGCTAGTGTGTGTTCTGTAAGCTGAGGTAACTCCGTTGGGGCTGTTAACG	4290
Db	10276	ACCTGAGTGTGTTCTGTAAGCTGAGGTAACTCCGTTGGGGCTGTTAACG	10335
Qy	4291	GTGGAGGGCGGTGAGCTGAGCACTCTGGTGTGCGGGCGGGCACAGACATAAT	4350
Db	10336	GTGGAGGGCGGTGAGCTGAGCACTCTGGTGTGCGGGCGGGCACAGACATAAT	10395
Qy	4351	AGCTGACAGCTAAGACTGAGCTTCTGAGTCAC	4402
Db	10396	AGCTGACAGCTAAGACTGAGCTTCTGAGTCAC	10447

Search completed: October 12, 2004, 14:38:29
 Job time : 2213 secs

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

OM nucleic - nucleic search, using sw model						
Run on:	October 12, 2004, 14:01:32 ;	Search time 23942 Seconds (without alignments) 11600.625 Million cell updates/sec				
Title:	US-09-996-128a-1					
Perfect score:	6408					
Sequence:	1 attctgcagatatcagcac.....tcttattttaaaaaacccgaa 6408					
Scoring table:	IDENTITY_NTC					
	Gapop 10.0 , Gapext 1.0					
Searched:	3470272 seqs, 21671516995 residues					
Total number of hits satisfying chosen parameters:	6940544					
Minimum DB seq length:	0					
Maximum DB seq length:	200000000					
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries					
Database :						
1: GenBank:*						
2: gb_ba:*						
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Pred. No. is the number of results predicted by chance to have a

RESULT 1
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LOCUS AX743953
DEFINITION Sequence 1 from Patent WO03031630.
ACCESSION AX743953
VERSION AX743953.1 GI:30722650
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
AUTHORS Fazio,V., Rinaldi,M., Sonzogni,L., Tonon,G. and Orsini,G.
TITLE Multi-cisronic vectors for gene transfer protocols
PATENT WO 03031630-A 1 17-APR-2003;
Keryos Spa (IT)

Qy 2618 GAGATCTGATATAGGTGACAGACGATATGGGCTATATGCCGATAGGGCACATCAG 2677
 Db 3599 CCGACTGGAAAGCGGCAGTGCSCGCACGCAATTAGTGAGTTAGCTCACTCATGG 3540
 Qy 2678 C-----TEGACATGCCATATGATATGATCACTATAGTGCATATGG 2725
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 Qy 2838 TAGACCCGAGTGTGACTGATTAGCTAGTATATAATAGTACATAGGGT 2897
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 Db 3059 GAAATGSCCGCTGGCATATGCCAACTACAGCTTACGGACTTTCTACTTGC 3000
 Qy 3198 AGTACATCTAGGATTAGTGTGCTTACCATGGTGGCGTTGGCTACACCA 3257
 Db 2999 AGTACATCTAGGATTAGTGTGCTTACCATGGTGGCTACACCA 2940
 Qy 3258 ATGGCGTGGATAGCGTTGACTCACGGGATTTCCAAAGCTCACCCTAGGCTCA 3317
 Db 2939 ATGGCGTGGATAGCGTTGACTCACGGGATTTCCAAAGCTCACCCTAGGCTCA 2880
 Qy 3318 ATGGCGTGGATAGCGTTGACTCACGGGATTTCCAAAGCTCACCCTAGGCTCA 3377
 Db 2879 ATGGCGTGGATAGCGTTGACTCACGGGATTTCCAAAGCTCACCCTAGGCTCA 2820
 Qy 3378 CCCGGTGGACCAATGGGGTAGGGTACGTGGAGGTATAAGGAGGTC 3437
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Qy 3678 GATGGTATAGCTTACGGTGTGGTTATGACCAATTAGGCAACTCCCTATG 3737
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 Db 1859 CACCAAGCTATAGCTGACAGACTACAGAGTGTCTTCATGGCTTTCAG 1800

RESULT 2
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 LOCUS AX743955
 DEFINITION Sequence 3 from Patent WO0301630.
 VERSION AX743955
 ACCESSION AX743955.1 GI:30722652
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ARTIFICIAL artificial sequences.
 REFERENCE
 AUTHORS Fazio, V., Rinaldi, M., Sonzogni, L., Tonon, G. and Orsini, G.
 TITLE Multi-cisronic vectors for gene transfer protocols
 JOURNAL Patent: WO 0301630 A3 17-APR-2003;
 Keryos SpA (IT)
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 Query Match
 Best Local Similarity 44.9%; Score 2878.4; DB 6; Length 7086;

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Oy	645	ACCATATTTGAAAMCCGTTCTGTAATGAGGAAGAACTCACGGGAGTCCA	704					
Db	7021	ACCATATTTGAAAMCCGTTCTGTAATGAGGAAGAACTCACGGGAGTCCA	6962					
Oy	705	TAGATGGCAGAGCTCTGGATGGCTGCTGGATCCGACTCGTCAACATCATAC	764					
Db	6961	TAGATGGCAGAGCTCTGGATGGCTGCTGGATCCGACTCGTCAACATCATAC	6902					
Oy	765	TATTAATTCCCTCTGTAAMATAAGCTTATCAGTGTGAACTCACATGAGTGAG	824					
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Db	6781	GCATTAAGCTCGTCAATAAAATCACTGCAATGAAACCCATTATCAGTGTGAG	6722					
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QY	825	TGATTCGGTGGAGAGGAGAATAGGTTTCAAGTGAAGAACTCACCATGAGTGCAC	884	QY	1905	GAGCGAGATAAAATAGTGTCTCTAGTGTAGGGTAGTGGACACACTTCAAGA	1964
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Db	6969	CGCTGAGCGAGAGGAGAATAGGTTTCAAGTGAAGAACTCACCATGAGTGCAC	6910	Db	6147	CGAGGCGATTCAGGATAGTGTCTCTAGTGTAGGGTAGTGGACACAGGACAC	6088
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Db	6909	ATGCAACCGGGGAGGAACTTCCAGGCACTACAACTGAGTGTAAAGGAATTA	6850	Db	6087	CGAGGCGATTCAGGATAGTGTCTCTAGTGTAGGGTAGTGGACACAGGACAC	6028
QY	1065	TTCTCTATACCTCGTAATGCTGTTCCGGATCGAGTGTGAGTACCATGCTC	1124	QY	2142	ACCCGAGACTGAGATACTACAGGAGTAGTGTAGGAAAGCCACCTCCGAGGA	2201
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Db	6789	ATCAGGAGTAGGATAAATGCTGATGGCTGGAGAGGAAATACTCGTCAGC	6730	Db	5967	GAGGGGAGGATAGTGTGAAAGGAGGAGGAGGAGGAGGAGGAG	5908
QY	1185	TAGCTGACCATCTCATCTGTAATCATCGTGTGGACAGCTTGTGAGTAA	1244	Db	2262	TTCCAGGGGAAACGCCGTTGCTGTTGCGGTTCCGACCTCTGATG	2321
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QY	1425	GTAAGCAGACGAGTTATGTTGATGATATATTGTTCTGTCACATCA	1484	QY	2501	ATTAACGGGTCTATGCTATAGCCATATAGGAGTTCGGTACATAC--TAC	2557
Db	6489	GTAAGCAGACGAGTTATGTTGATGATATATTGTTCTGTCACATCA	6469	Db	5667	GCAGCCGACGACGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG	5608
QY	1485	GAGTTTGAGACAAACGTTGGCTTCCCCCCCCCTGAGGGTTCTCTT	1544	QY	2558	GTTAAATGGCCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	2617
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Db	6468	AATTAAGGAGTAGGAGATCTTGTAACTCATGACAAATCCCTAAC	6468	Db	5487	CACCCAGGCTTACACTTATCGCTGCTGCTGCTGCTGCTGCTG	5428
QY	1725	GTGAGTTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG	1784	QY	2725	--CAATAGCCATTAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG	2777
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QY	2838	TATGACCGCCATGTTGACATTGATTGATTGACTGTTAATAGTA	2897	QY	2838	TATGACCGCCATGTTGACATTGATTGATTGACTGTTAATAGTA	2897

QY	1855	GGGGGATCAAGAGCTAACACTTTTCCGAGAGCTACTGGTTACAGAGCGCGAT	1914	Db	2387	CATTAGTCATGCCCATATATGGAGTCCGGTTAATACATTACGGTAATGGCCCG	2957
Db	1307	GGGGGATCAAGAGCTAACACTTTTCCGAGAGCTACTGGTTACAGAGCGCGAT	1366	Qy	2958	CCTGGCTAACGCCAACAGACCCCGCCCATTCAGTCATATGAGCTAATGTCATAG	3017
Qy	1915	ACCAAACTGTGTTCTCTAGTGTAGCTAGCCCTAGTGTAGGCACCACTCTGTG	1974	Db	2447	CTCG-TACCGCCAACACCCCGCCATTCAGTCATATGACCTATGTCATAG	2505
Db	1367	ACCAAACTGTCTCTAGTGTAGCCCTAGTGTAGGCACCACTCTGTAG	1426	Qy	3018	TAACGCCATATGGACTTTCCATGAGCTCAATGGGGAGTATTACGGTAATGCGCC	3077
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Db	1487	CTGGTCTCTACCGGGTGTGGACTCAAGAGCATGTGTACCGGATAAGGGCAGCGTGG	1546	Qy	3137	GTAAATGCCCCCTGGCATATGCCAGTCAGCTGGCTGCTGCCCTATGACCTCAATG	3196
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Qy	2155	ATACCTACAGGGTGTGGACTATGAGAAGGGCAGCGTGGCTGCTGCCAGGAGAAGG	2214	Db	2686	CAGTACATCTGCTGGCATATGCCAGTCAGCTGGCTGCTGCCCTATGACCTCAATG	2745
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Qy	2215	GTATCGGTAAGGGCAGGGTCGAGAAGGGAGGGCAGCGTGGCTGCTGCCAGGAG	2274	Db	2746	ATGGGCGTAGGGTAGGGTTTACTCACGGGAATTTCAGGTTCACCCCATGAGTC	2805
Db	1667	GTATCGGTAAGGGCAGGGTCGAGAAGGGAGGGCAGCGTGGCTGCTGCCAGGAG	1726	Qy	3317	ATGGGAGTTTTGGCACAAATCACCGGACTTCCAAATGPTGATAACCC	3376
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Db	1907	TGTGGTACCGTATACGCCATGCGATTAGTTAATGAGTCACCGGAAAGGAGATGAG	1966	Qy	3497	AGACACCGGACGATCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC	3556
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RESULT 6
 AX776821 LOCUS AX776821
 DEFINITION Sequence 3 from Patent WO03004055.
 VERSION AX776821.1 GI:32694263
 KEYWORDS SOURCE unidentified
 ORGANISM unclassified.

REFERENCE 1
 AUTHORS Haynes, J.R. and Arrington, J.E.
 TITLE Nucleic acid adjuvants
 JOURNAL Patent: WO 03004055-A 3 16-JUN-2003;
 PowderJect Vaccine, Inc. (US)

FEATURES source
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ORIGIN

Query Match 37.1%; Score 2378; DB 6; Length 5488;
 Best Local Similarity 91.6%; Pred. No. 0; Mismatches 197; Indels 41; Gaps 6;
 Matches 2598; Conservative 0; Mismatches 197; Indels 41; Gaps 6;

QY 1615 AGCTCAAGTACTCATATAACTTGGATGATGATTAACCTCATTTTAAAG 1674
 Db 1067 AGCAAGTACTCATATAACTTGGATGATGATTAACCTCATTTTAAAG 1126
 QY 1675 GATCTAGTGGAGATCTTGGATATCTCATGACCAAATCCCTAACGGTGGTTTC 1734
 Db 1121 GATCTAGTGGAGATCTTGGATATCTCATGACCAAATCCCTAACGGTGGTTTC 1186
 QY 1735 GTTCACTGAGGTAGACCCGGTAGAAGTCAGGAGTCTCTGAGATCCCTTT 1794
 Db 1187 GTTCACTGAGGTAGACCCGGTAGAAGTCAGGAGTCTCTGAGATCCCTTT 1246
 QY 1795 TCTGGGGAATCTGCTTGCACAAACAAACACCGTACACAGGGTGGTTTT 1854

QY	3977	GGCCTTTCCTCGGTTGGGGGAGGTTCCACATCGGACCTGCTGCTTCATGCCCCACCGG	4036	Db
Db	3465	GGCTTCTTCGTTGGGGGAGGTTCCACATCGGACCTGCTGCTTCATGCCCCACCGG	3524	Db
QY	4037	GCTCCTGGTGCCTGGGGAGGTTCTGCTCTAACGTTGGGGGAGGTTGGGAGGCA	4096	Db
Db	3525	GCTCCTGGTGCCTGGGGAGGTTCTGCTCTAACGTTGGGGGAGGTTGGGAGGCA	3584	Db
QY	4097	CAATGCCACACCCCAAGTGGGGGAGGTTCTGCTCTAACGTTGGGGGAGGTTGGGAGGCA	4156	Db
Db	3585	CAATGCCACACCCCAAGTGGGGGAGGTTCTGCTCTAACGTTGGGGGAGGTTGGGAGGCA	3644	Db
QY	4157	ATGAGCTCGAGATGGGGTGGGGCTGCGAGCTGGGGTGTGTTGTTGAGGAGCTTAA	4216	Db
Db	3645	ATGAGCTCGAGATGGGGTGGGGCTGCGAGCTGGGGTGTGTTGAGGAGCTTAA	3703	Db
QY	4217	AAGAGATGAGGAGCTGGGGCTGCGAGCTGGGGTGTGTTGAGGAGCTTAA	4276	Db
Db	3704	AAGAGATGAGGAGCTGGGGCTGCGAGCTGGGGTGTGTTGAGGAGCTTAA	3763	Db
QY	4277	CGGCTGTGTAACGCTGGGGGAGGTTGGGGGAGGTTGGGGTGTGTTGAGGAGCTTAA	4336	Db
Db	3764	CGGCTGTGTAACGCTGGGGGAGGTTGGGGGAGGTTGGGGTGTGTTGAGGAGCTTAA	3823	Db
QY	4337	CCACCAAGACATAATGGTGGAGGAGTAACGACTTCTTCCATGGGCTTCTGCA	4396	Db
Db	3824	CCACCAAGACATAATGGTGGAGGAGTAACGACTTCTTCCATGGGCTTCTGCA	3883	Db
QY	4397	GTCAACGGTCCACCGCT 4412		Db
Db	3884	GTCAACGGTCCACCGCT 3899		Db
RESULT 7				
AX776824				
LOCUS	AX776824	5498 bp	DNA	linear
DEFINITION	Sequence 6 from Patent WO03004055.			PAT 14-JUL-2003
ACCESSION	AX776824.1	GI:32694266		
VERSION				
KEYWORDS	unidentified			
SOURCE	unidentified			
ORGANISM	unclassified			
FEATURES				
REFERENCE	1			
AUTHORS	Haynes, J.R. and Arrington, J.E.			
TITLE	Nucleic acid adjuvants			
JOURNAL	Patent: WO 03004055-A 6 16-JAN-2003;			
POWERJECT	Vaccines, Inc. (US)			
LOCATIONS/QUALIFIERS				
SOURCE	1. .5488			
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/note="PPJV2007 plasmid"				
ORIGIN				
Query Match	37 1%; Score 2378.8;	DB 6;	Length 5488;	
Best Local Similarity	91 6%; Pred. No. 0;			
Matches 2598; Conservative	0; Mismatches	197; Indels	41; Gaps	6;
QY	1615	AGCCCTGAGGTTACTATATATCTTGTAGTGTAACTCTTAACTTAAAG	1674	Db
Db	1067	AGCCCTGAGGTTACTATATATCTTGTAGTGTAACTCTTAACTTAAAG	1126	Db
QY	1675	GATCTAGGTGAGACCTTTGATAATCTCATGCCAACATCCCTAACGTGAGTTTC	1734	Db
Db	1127	GATCTAGGTGAGACCTTTGATAATCTCATGCCAACATCCCTAACGTGAGTTTC	1186	Db
QY	1735	GTTCGACTGAGCGTGAACCCCGTGAACAAAGATCAAGAGTCTTGTAGATCTT	1794	Db
Db	1187	GTTCGACTGAGCGTGAACCCCGTGAACAAAGATCAAGAGTCTTGTAGATCTT	1246	Db
QY	1915	ACCAAACTGTCCTCAGTGTAGGCTAGGGCCACCTCAAGAACCTGTCAG	1974	Db
Db	1367	ACCAAACTGTCCTCAGTGTAGGCTAGGGCCACCTCAAGAACCTGTCAG	1426	Db
QY	1975	ACCCGCTACATACCTCGCTGCTGCTATCCCTGTTACCGTGTGAGGATAA	2034	Db
Db	1427	ACCGCTACATACCTCGCTGCTGCTATCCCTGTTACCGTGTGAGGATAA	1486	Db
QY	2095	CTGAACGGGGGGTCTGTCAGACAGCTTACGGATAAGCCAGGTCGCG	2154	Db
Db	1547	CTGAACGGGGGGTCTGTCAGACAGCTTACGGATAAGCCAGGTCGCG	1606	Db
QY	2155	ATACCTACAGGTGAGCTTGTAGAAGACGACTTACGGATAAGGGCAAGGAG	2214	Db
Db	1607	ATACCTACAGGTGAGCTTGTAGAAGACGACTTACGGATAAGGGCAAGGAG	1666	Db
QY	2215	GTATCGGTAGCGCAGGGTGGAGGAGCTCCGGAGGGAAAGGGAGA	2274	Db
Db	1667	GTATCGGTAGCGCAGGGTGGAGGAGCTCCGGAGGGAAAGGGAGA	1726	Db
QY	2275	GCCTCTGTATCTTATAGTCCTGTCGGGTTGCCACCTCTGACTTGTAGGCTGCA	2334	Db
Db	1727	GCCTCTGTATCTTATAGTCCTGTCGGGTTGCCACCTCTGACTTGTAGGCTGCA	1786	Db
QY	2335	GTGAGTGTCTCTGAGGGGGGGAGGCTATGGAAACGCGACAGCGCCTTTAG	1846	Db
Db	1787	GTGAGTGTCTCTGAGGGGGGGAGGCTATGGAAACGCGACAGCGCCTTTAG	1846	Db
QY	2395	GTTCCTGGCCTTGTGGCTTGTGAGTGTAACTGTCTTCTGGTATCCCTGATC	2454	Db
Db	1847	GTTCCTGGCCTTGTGGCTTGTGAGTGTAACTGTCTTCTGGTATCCCTGATC	1906	Db
QY	2455	TGTGAACTACGGTATTACGGCATGCAATTAGTAACTGTAACTGTAACTGTAA	2505	Db
Db	1907	TGTGAACTACGGTATTACGGCATGCAATTAGTAACTGTAACTGTAACTGTAA	1966	Db
QY	2506	CGGGCTCATGGTGTAGCCATAGCCCATATAGGATTCGGCTTACATACTTCGTA	2555	Db
Db	1967	CGGGCTCATGGTGTAGCCATAGCCCATATAGGATTCGGCTTACATACTTCGTA	2026	Db
QY	2566	GGCCCGCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2620	Db
Db	2027	GGCCCGCTGAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG	2086	Db
QY	2621	-----ATCTGATATAGGTGACAGGCAATGAGCTTGTGAGCTTGTGAGCTTGT	2657	Db
Db	2087	GGGCACTGAGGGCAACGCAATTATGGTGTAGTGTAGCTCATGCTTACGGCTT	2146	Db
QY	2658	CGATAGAGGGACATCAAGCTGGCACATGCCATGCAATGCACTTACATGATC	2717	Db
Db	2147	ACACTTATGCTCGGTGTAGTGTGAGGTTGTGAGCTTGTGAGCTTGTGAGCTT	2206	Db
QY	2718	ATATATGGCAATTACGGTATAGGATGGCTTATAGGATTAATCAATAATGGCTT	2777	Db
Db	2207	AGGAAACAGCTATGACCATGATGAGCTTGTGAGCTTGTGAGCTTGTGAGCTT	2266	Db
QY	2778	GGCCATGCACTGGTGTAGTGTGAGCTTGTGAGCTTGTGAGCTTGTGAGCTT	2837	Db
Db	2267	GGCCATGCACTGGTGTAGTGTGAGCTTGTGAGCTTGTGAGCTTGTGAGCTT	2326	Db
QY	2838	TATGACGCCATGGTGTAGTGTGAGCTTGTGAGCTTGTGAGCTTGTGAGCTT	2897	Db

Qy	2674	CAAGTGGCACATGCCAATGCAATCGATCTATACATGAMTCATAATTGCAATTAGC	2733	Db	9266	TTACTAATCCATACATGGCTTGGCACAACTATCTTATGGCTATGCCAATACT	9325		
Db	8278	-----	-----	Db	8277	-----	-----		
Qy	2734	CATATTAGTCATGGTTATAGCATATAATCAATTGGCTATGGCAATTGCTATAGCTT	2793	Qy	3814	CTGTCTCTCAAGAGCTGAGCAAGGACTCTGTATTTCAGATGGGGTCATTATAT	3873		
Db	8278	-----	-----	Db	9326	CTGTCTCTCAAGAGCTGAGCAACGGCTCATGGCTATAGCTTATAGCTTATAT	9385		
Qy	2794	GTATCTATATCATATAATGACATTTATGGCTATGTCCTATGACGCCATGTG	2853	Qy	3874	TTACAATTCACTACACACACGGCTCCCGCAGTTTAACTAACATAG	3933		
Db	8309	GTATCTATATCATATAATGACATTTATGGCTATGTCCTATGTCCTATAGCTT	8368	Db	9386	TTACAATTCACTACACACACGGCTCCCGCAGTTTAACTAACATAG	9445		
Qy	2854	ACATGTGATTGACTAGTATTAACTAACTAGGAAATGGGCTATTAGTCATAGCC	2913	Qy	3834	CTGGGGATCTCCACCGCAATCTGGGTACGTTCCGACATGGCTCTCCGGTAGC	3993		
Db	8369	ACATGTGATTGACTAGTATTAACTAACTAGGAAATGGGCTATTAGTCATAGCC	8428	Db	9446	CTGGGGATCTCCACCGCAATCTGGGTACGTTCCGACATGGCTCTCCGGTAGC	9505		
Qy	2914	ATATATGGAGTCGGGTTACATAACTACGGTAATGCCCGCTGCTGACGGCCAA	2973	Qy	3894	GGGGGACTTCCACATCGACGGCTGGCCCTGCTCCATGCTCCAGGGCTATGTCGCGC	4053		
Db	8429	ATATATGGAGTCGGGTTACATAACTACGGTAATGCCCGCTGCTGACGGCCAA	8487	Db	9506	GGCGGACTTCCACATCGACGGCTGGCCCTGCTCCATGCTCCAGGGCTATGTCGCGC	9565		
Qy	2974	CGACCCCCCCCCATGGCTAATGATGAGGTAATGTTCCCTAGTAAGGCCATAGGGAC	3033	Qy	4054	AGTCTCTGCTCTAAGGTGGAGGAGACTTAGCCAGCACATGCCACACCCACC	4113		
Db	8488	CGACCCCCCCCATGGCTAATGACGCTATAATGACGTAATGAGTCCATAGGAC	8547	Db	9566	AGCTCTCTGCTCTAAGGTGGAGGAGACTTAGCCAGCACATGCCACACCCACC	9625		
Qy	3034	TTTCCATTGAGCTAATGGGGTATTACGGTAATGCGACTTGGCAGTACATCA	3093	Qy	4114	AGTGTGGCGCAAGGGCGTGGGGTAGGGTATGCTGAATAGCTGGAGATTTG	4173		
Db	8548	TTTCCATTGAGCTAATGGGGTATTACGGTAATGCGACTTGGCAGTACATCA	8607	Db	9626	AGTGTGGCGCAAGGGCGTGGGGTAGGGTATGCTGAATAGCTGGAGATTTG	9685		
Qy	3094	AGTGTATCATTCGAACCTCGCCCTTATGAGTCATGAGGTAATGCCCGCTG	3153	Qy	4174	GTGTCGCGCTGAGGAGATGGCTAAGGAGCGGAGAAGAGATGGCAGGAGC	4233		
Db	8608	AGTGTATCATTCGAACCTCGC-CCCCTATGAGTCATGAGGTAATGCCCGCTG	8666	Db	9686	GTGTCGCGCTGAGGAGATGGCTAAGGAGCGGAGAAGAGATGGCAGGAGC	9744		
Qy	3154	GCATATTGCCCCAGTACATGACCTAACGGCTTCCACTGGCAGTACATCACTGTT	3213	Qy	4224	TGAGTGTGTATTCTGATAGAGTCAGGTAATCCCTGGCTGCTTTAAGGGT	4293		
Db	8667	GCATATTGCCCCAGTACATGACCTAACGGCTTCCACTGGCAGTACATCACTGTT	8726	Db	9745	TGAGTGTGTATTCTGATAGAGTCAGGTAATCCCTGGCTGCTTTAAGGGT	9804		
Qy	3214	AGTCATCGCTTACCATGGTGTGGGTTTGCACTGAGCTTACGGCTTCTACTGGCAGTACATCA	3273	Qy	4224	GGGGCGCTGAGTCTGAGCACTGAGCTACTGTTGCTGCCCCGGGGGGGACAGATAATAGC	4353		
Db	8727	AGTCATCGCTTACCATGGTGTGGGTTTGCACTGAGCTTACGGCTTCTACTGGCAGTACATCA	8786	Db	9805	GGGGCGCTGAGTCTGAGCACTGAGCTACTGTTGCTGCCCCGGGGGGGACAGATAATAGC	9864		
Qy	3274	GTGTTGACTTCACGGGATTTCAGTCAGTCACCCATGAGCTCAATGGGAGTTGTTG	3333	Qy	4354	TGACAGACTAACAGACTGTTCCATGGCTCTTCAGGTCAGTCACCGTCA	4407		
Db	8787	GTGTTGACTTCACGGGATTTCAGTCAGTCACCCATGAGCTCAATGGGAGTTGTTG	8846	Db	9865	TGACAGACTAACAGACTGTTCCATGGCTCTTCAGGTCAGTCACCGTCA	9918		
Qy	3334	GCACCAAAATCAAGGGACTTCCAAAATGCTGATAACCCCCGGGCTGCGCAAT	3393	RESULT 11					
Db	8847	GCACCAAAATCAAGGGACTTCCAAAATGCTGATAACCCCCGGGCTGCGCAAT	8906	AXI138932	AXI138932	Sequence 51 from Patent EP1052286.	5108 bp	DNA	linear
Qy	3394	GGGGCGCTGAGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTA	3453	DEFINITION	Sequence 51 from Patent EP1052286.	PAT 31-MAY-2001			
Db	8907	GGGGCGCTGAGGCTTACGGCTTACGGCTTACGGCTTACGGCTTACGGCTA	8966	ACCESSION	AXI138932	AXI138932.1	GI:14274637		
Qy	3454	GATGCGCTGAGAGGCCATTCAGCTGTTGACTCCATAGAGACACGGGACGGTC	3513	VERSION	AXI138932.1	GI:14274637			
Db	8967	GATGCGCTGAGAGGCCATTCAGCTGTTGACTCCATAGAGACACGGGACGGTC	9026	KEYWORDS					
Qy	3514	CAGCTCCGGGGGGGAAGGGCTTACGGCTTACGGCTTACGGCTTACGGCTA	3573	SOURCE					
Db	9027	CAGCTCCGGGGGGGAAGGGCTTACGGCTTACGGCTTACGGCTTACGGCTA	9086	ORGANISM					
Qy	3574	AAGTACCGCTTATGACTCTATGGCAACCCCTTGGCTTACGGCTTACGGCTT	3633	FEATURES					
Db	9087	AAGTACCGCTTATGACTCTATGGCAACCCCTTGGCTTACGGCTTACGGCTT	9146	REFERENCE					
Qy	3634	TTGGCTTGGGGCTTACACCCCTTGGCTTACGGCTTACGGCTTACGGCTA	3693	AUTHORS	Morse, M.A. and Shoppard, M.G.				
Db	9147	TTGGCTTGGGGCTTACACCCCTTGGCTTACGGCTTACGGCTTACGGCTA	9205	TITLE	Growth hormone and growth hormone releasing hormone compositions				
Qy	3694	CTATAGTGTGGGTATTGACCATATTGGCACTCCCTATTGGAGACTTCGA	3753	JOURNAL	Patent: EP 1052286-A 51-15-Nov-2000;				
Db	9206	CTATAGTGTGGGTATTGACCATATTGGCACTCCCTATTGGAGACTTCGA	9265	Pfizer Products Inc. (US)					
Qy	3754	TTACTAATCCATAACATGGCTTTCGACCAACTATCTTATGGCTATATGCCAATCT	3813	LOCATION	Location/Qualifiers				
			ORIGIN						
			Query Match						
			Best Local Similarity						
			Matches 3058; Conservative						
			0; Mismatches 239; Indexes 826; Gaps 8;						
			Query						
			287 GGGGGGGGGGGCTTGGCTTGGAGAGGGTGTGCTGACTCATACGGCC						
			346						

Db	1562	GGGGGGGGGGGGCTGAGGTCTGCTCGTAAGAGGTGTTGCTGACTCATACAGCC	1621	QY
QY	347	TGAATGCCCATCATCCGCCAGAAGTGGAGGGCCGGTGTAGAGGCTTGTG	406	Db
Db	1622	TGAATGCCCATCATCCGCCAGAAGTGGAGGGCCGGTGTAGAGGCTTGTG	1681	QY
QY	407	TAGGTGGACCAAGTGTGATTTGAGCTTGTGCTTGCTTGAGGAGGCGGCTG	466	Db
Db	1682	TAGGTGGACCAAGTGTGATTTGAGCTTGTGCTTGCTTGAGGAGGCGGCTG	1741	QY
QY	467	GGGAGATGGTGTGATCTGACTCTCAACTCGAACAAAGTGGATTATCAACAAAGGCC	526	Db
Db	1742	GGGAGATGGTGTGATCTGACTCTCAACTCGAACAAAGTGGATTATCAACAAAGGCC	1801	Db
QY	527	CGTCGGTCAAGTCAGTCAGCTATGCTCTGCCAGGTTACACCGAACGGCTG	586	Db
Db	1802	CGTCGGTCAAGTCAGTCAGCTATGCTCTGCCAGGTTACACCGAACGGCTG	1861	QY
QY	587	AGAAAACCTCATGAGCATCAATGAGCTTGTGCTTGAGGAACTTGTGATT	646	Db
Db	1862	AGAAAACCTCATGAGCATCAATGAGCTTGTGCTTGAGGAACTTGTGATT	1921	QY
QY	647	CATATTGAAAGGCCCTTCTGTAAGTGAAGGAAACTTACGGGAGTCCATA	706	Db
Db	1922	CATATTGAAAGGCCCTTCTGTAAGTGAAGGAAACTTACGGGAGTCCATA	1861	QY
QY	707	GGATGGCAAGATCTGGATCGGCTGCAATTGAACTTACGGGAGTCCATA	766	Db
Db	1982	GGATGGCAAGATCTGGATCGGCTGCAATTGAACTTACGGGAGTCCATA	2041	QY
QY	767	TTAATTCCCTCGTCAGATAAAATAGTTTCACTGAGAATTCAGGATTAACCA	826	Db
Db	2042	TTAATTCCCTCGTCAGATAAAATAGTTTCACTGAGAATTCAGGATTAACCA	2101	QY
QY	827	AATCCGGGAGAATGGCAAAAGCTATCATTCTTCCAGACTGTGTCACGCC	886	Db
Db	2102	AATCCGGGAGAATGGCAAAAGCTATCATTCTTCCAGACTGTGTCACGCC	2161	QY
QY	887	CATACGCTGTCATCAAAATCACTCGCTACCAACGGTTATCCTGTAATGG	946	Db
Db	2162	CATACGCTGTCATCAAAATCACTCGCTACCAACGGTTATCCTGTAATGG	2221	QY
QY	947	CCTGAGCGAGACGAAATACCGATGCTGTTAAAGGACATTACAAAGGGATGAT	1006	Db
Db	2222	CCTGAGCGAGACGAAATACCGATGCTGTTAAAGGACATTACAAAGGGATGAT	2281	QY
QY	1007	GCAACCGGCGAGAACACTGCGCGCATCAACATAATTTCACCGATATCGGAT	1066	Db
Db	2282	GCAACCGGCGAGAACACTGCGCGCATCAACATAATTTCACCGATATCGGAT	2341	QY
QY	1067	CTCTAACTCTGGAAATGCTGTTCCCGGGATGCGAGTGTGAGTACATCGCAT	1126	Db
Db	2342	CTCTAACTCTGGAAATGCTGTTCCCGGGATGCGAGTGTGAGTACATCGCAT	2401	QY
QY	1127	CAGGAGTACGATAAAATCTGATGGTGGAGGGATTAATCCGTAGCGATT	1186	Db
Db	2402	CAGGAGTACGATAAAATCTGATGGTGGAGGGATTAATCCGTAGCGATT	2461	QY
QY	1187	GTCGACCATCTCTGACATCGAACGCTACCTTGGCAGTTGAGAACACA	1246	Db
Db	2462	GTCGACCATCTCTGACATCGAACGCTACCTTGGCAGTTGAGAACACA	2521	QY
QY	1247	ACTCTGGCCATCGGCTCCCATACATCGATGAGATGCTGGCACTGATGCCGAT	1306	Db
Db	2522	ACTCTGGCCATCGGCTCCCATACATCGATGAGATGCTGGCACTGATGCCGAT	2581	QY
QY	1307	TATCCGGAGCCATTATACCCATAATTCAGATCCATGTTGGATTAATCCGCGC	1366	Db
Db	2582	TATCCGGAGCCATTATACCCATAATTCAGATCCATGTTGGATTAATCCGCGC	2641	QY
QY	1367	TCGAGCAAGCGTTCCCGTGAATATGGCTCATACACCCCTGTTATCTGTTATG	1426	Db
Db	2642	TCGAGCAAGCGTTCCCGTGAATATGGCTCATACACCCCTGTTATCTGTTATG	2701	QY

QY	2507	GGGGTCATTTAGTTTCAATAGCCCCATATATGGAGTTCCGGGTTACATAACTTACCGTAATGG	2566	Db	4036	AGACTCTATAGGCACACCCCTTGGCTCTTGTCACTATAGCTTGTGCTTGGGC	4095
Db	3100	-----	-----	-----	4047	CTATACCCCCCGCTCTTTAGTCTTAGGGATGTTATGTTACCTTAAAGGTGTTGGG	3706
QY	2567	CCGCCTCGGTGACCCGCCAACCAACCCCGCCCATGAGTCATAATGAGCAGATCTGA	2626	Db	4196	CTATACCCCCCGCTCTTTAGTCTTAGGGATGTTAGGTGATGGTATGGTTCCTATAGGTTGGG	4155
Db	3113	CGGGCTCGCTTAACATAGCGGATCAGAGCAGATGGTACTGAGAGTCACCCATATGGG	3172	QY	3107	TTATGACCATTTGGCCTCCCTATGGTACAGTCTTCCATAGCTTCAATATCCATA	3766
QY	2627	TATAGGTGACAGAGATAGTGGAGCTATGAGCTATATGCCGATAGAGGGCACATCAAGCTGGCAT	2686	Db	4156	TTATGACCATTTGGCCTCCCTATGGTACAGTCTTCCATAGCTTCAATATCCATA	4215
Db	3173	TGTGAAATACCCGACAGATGGG-----	-----	QY	3167	ACATGGCTTGGCAAGAACATCTCTTATGGCTATATGCCAATACTCTGCTCTTAGAG	3826
QY	2687	GSCCAATGCAATCGATCTTACATGGATCAATATGGCAATTAGGCATATTAGTCATT	2746	Db	4216	ACATGGCTTGGCAAGAACATCTCTTATGGCTATATGCCAATACTCTGCTCTTAGAG	4275
Db	3195	-----	-----	QY	3127	ACTGACAGGACTCTGATTTCAGAGATGGGTCATATGCCAATACTCTGCTCTTAGAG	3886
QY	2747	GGTATATAGCATATCATATGCTATGGCATAGCTTATGGTATATCAT	2806	Db	4276	ACTGACAGGACTCTGATTTCAGAGATGGGTCATATGCCAATACTCTGCTCTTAGAG	4275
Db	3196	AAGGAGAAATACCGCATAGATGGCATATGCCATAGCTTATGGTATATCAT	3255	QY	3887	TATACACAAACCGCGTCCCCCGTGCAGCTTTATAACATAGGTGGGATCTCA	3946
QY	2807	AATATGACATTATATGGCTATGTCATAGTCATATGACGCCATGTTGACATGATGATTG	2866	Db	4336	TATACACAAACCGCGTCCCCCGTGCAGCTTTATAACATAGGTGGGATCTCA	4395
Db	3256	AATATGACATTATATGGCTATGTCACATTACCGCATGTGACATGATGATTG	3315	QY	3947	CGGAATTCGCGGTACCTGGTTCGGAAATGGCTTCTCGGTAGGGGGAGCTTCA	4006
QY	2867	ACTAGTAAATAGTAACTAACATACCGTAAATGGCCGCGTGGCTGACCGCCAAAGAACCCGGCCA	2926	Db	4396	CGCGAATTCGCGGTACCTGGTTCGGAAATGGCTTCTCGGTAGGGGGAGCTTCA	4455
Db	3316	ACTAGTAAATAGTAACTAACATACCGTAAATGGCCGCGTGGCTGACCGCCAAAGAACCCGGCCA	3375	QY	4007	CATCGGACCCMGTGTCATGCTCCAGGCTATGCTCAGGAGCTCTGCTC	4066
QY	2927	CGCGTACATAACTTACCGTAAATGGCCGCGTGGCTGACCGCCAAAGAACCCGGCCA	2986	Db	4456	CATCGGACCCMGTGTCATGCTCCAGGCTATGCTCAGGAGCTCTGCTC	4515
Db	3376	CGCGTACATAACTTACCGTAAATGGCCGCGTGGCTGACCGCCAAAGAACCCGGCCA	3435	QY	4067	TAACAGTGGAGCCAGACTAGGCACAGTCATGGCTTCTCGGTAGGGGGAGCTTCA	4126
QY	2987	TGAGCTATGAGCCTATGTTCCATAGTAACTGGACTTTCTATGGAT	3046	Db	4516	TAACAGTGGAGCCAGACTAGGCACATGGCTTCTCGGTAGGGGGAGCTTCA	4575
Db	3436	TGAGCTGAAATAATGACCTATGACCTATGTCCTCCATAGTAACTGGACTTTCTATGGAT	3495	QY	4127	AGGGCGTGGGTAGGGTATGGCTCAAATGAGTCGGAGATGGCTGGCTCACCGCT	4186
QY	3047	CAATGGGTGAGTTTACGGTAACCTGGCCATCTGGAGTAGTCAATCAAGTGTATG	3106	Db	4576	AGGGCGTGGGTAGGGTATGGCTCAAATGAGTCGGAGATGGCTGGCTCACCGCT	4635
Db	3496	CAATGGGTGAGTTTACGGTAACCTGGCCATCTGGAGTAGTCAATCAAGTGTATG	3555	QY	4187	ACCGAGTGGAAAGACTTAACTGGAGCTGAGGAGAGTGGAGCTGGAGTGTAT	4246
QY	3107	CCAGTCGCCCTATGGACGCTAATGACGTAATGGCCCGCTGCGATATGGCCAG	3166	Db	4636	ACCGAGTGGAAAGACTTAACTGGAGCTGAGGAGAGTGGAGCTGGAGTGTAT	4695
Db	3556	CCAGTAGCCCCCTATGGACGCTAATGACGTAATGGGGTAATGCCCGCTGGCATATGGCCAG	3615	QY	4247	TCTGATAGAGTCAGAGCTTCTGGGGGGGGGACAGGAGATACTGGAGCTGGTAG	4306
QY	3167	TACATGACCTTACGGACCTTCTACTGGCAGTACATCTCGTATAGTCATGCTATT	3226	Db	4696	TCTGATAGAGTCAGAGCTTCTGGGGGGGGGAGCTGAGTGTATGGAGGCGAGCTG	4755
Db	3616	TACATGACCTTACGGACCTTCTACTGGCAGTACATCTCGTATAGTCATGCTATT	3675	QY	4307	TCTGAGGAGTACTCTGGCTGGGGGGGGGACAGGAGATACTGGAGCTGAGTACA	4366
QY	3227	ACCATGGGTGATGGCGTTTGGCAGTACACCAATGGCGTGGGATAGGGTTGACTCAGG	3286	Db	4756	TCTGAGGAGTACTCTGGCTGGGGGGGGGACAGGAGATACTGGAGCTGAGTACA	4815
Db	3676	ACCATGGGTGATGGCGTTTGGCAGTACACCAATGGCGTGGGATAGGGTTGACTCAGG	3735	QY	4367	GACTGTCTTTCATGGCTTCTGGGGCTTCTGGCAGTCACCCCTCAGG	4409
QY	3287	GGATTCCAAGTCTCACCCCATGGCAGTACATGGAGTTGGTTGGCACCACCAAATCAA	3346	Db	4816	GACTGTCTTTCATGGCTTCTGGGGCTTCTGGCAGTCACCCCTCAGG	4958
Db	3736	GGATTCCAAGTCTCACCCCATGGCAGTACATGGAGTTGGTTGGCACCACCAAATCAA	3795	RESULT 12			
QY	3347	GGGGACTTCCAAATGGGTAATACCCGCCCGTGAAGAACATGGGGTAGGGT	3406				
Db	3796	CGGGACTTCCAAATGGGTAATACCCGCCCGTGAAGAACATGGGGTAGGGT	3855	AK138933	AK138933	Sequence 52 from Patent BP1052286.	5108 bp
QY	3407	GTAGCGTGGAGGCTATTAAGCAGAGCTCGTTAGTGAACCTCAGATCGCTGGAGA	3466	DEFINITION	VERSION	ACCESSION	DNA
Db	3856	GTAGCGTGGAGGCTATTAAGCAGAGCTCGTTAGTGAACCTCAGATCGCTGGAGA	3915	AK138933	AK138933.1	GI:1424638	LINEAR
QY	3467	CGCATCCAGCTGGCTTGGACGCTCCATAGAGGACCCGACCGATCCAGGCTTCCGGCG	3526	KEYWORDS	ORGANISM	Synthetic construct	PAT 30-MAY-2001
Db	3916	CGCCATCCAGCTGGCTTGGACGCTCCATAGAGGACCCGACCGATCCAGGCTTCCGGCG	3975	REFERENCE	ORGANISM	artificial sequences.	
QY	3527	CGGAAACGGTGCATGGAAAGGGATTCCCGTCAAGAGTGAAGTACCGCTT	3586	AUTHORS	REFERENCE	Morsey, M.A. and Sheppard, M.G.	
Db	3976	CGGAAACGGTGCATGGAAAGGGATTCCCGTCAAGAGTGAAGTACCGCTT	4035	TITLE	AUTHORS	Growth hormone and growth hormone releasing hormone compositions	
QY	3587	AGACTCTATAGGCACACCCCTTGGCTTATGCTGTTGGCTTGGGC	3646	JOURNAL	TITLE	Patent: EP 1052286 A 52 15-Nov-2000;	
				FEATURES	ORGANISM	Pfizer Products Inc. (US)	
				source	ORGANISM	Location/Qualifiers	
					1		

Db	2936	-	2935
Qy	1967	TCTGTAGCACGCCCTACATACCTCGCTCTGCTAATCCCTGTACAGTGCTGCTGCCAGT	2026
Db	2936	-	2969
Qy	2027	GGCCTATAAGTCGTTCTTACCGGGTTGAACTCAAGACGATAGTTACCGGTAAGGCGAG	2086
Db	2970	GCCTTTCCTCT-	2982
Qy	2087	CGGTTGGCTGAAACGGGGGTTCTGCAACAGGCCACGTTGGAGGAAACGACCTACACC	2146
Db	2983	-	2982
Qy	2147	GAAGTGGATACTACAGGGGAACTATGAGAAGGCCAACGCTTCCGAGGAGAAG	2206
Db	2983	-	3036
Qy	2207	GGGGACAGGTTACCGGTAAGGGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGCTCCA	2266
Db	3037	GGTCACAGCTGTCGTGTAAGCGG-ATGCGGGACAGAACGCCGTCAGGGCGTAG	3095
Qy	2267	GGGCGAAACGCCCTGTTATAGTCCTGTCGGTTGCCACCTGTACTTGAGGCT	2326
Db	3096	CGGG-----	3099
Qy	2327	CGATTTGATGCTCGTCAGGGGGCGAGCTATGGAAAAGCCAGAACGGGCC	2386
Db	3100	-	3099
Qy	2387	TTTTAACGGTTCTGGCTTTGGCTCATAGTCTTCTGCGTTACATTAC	2446
Db	3100	-	3099
Qy	2447	CTCTGATTCTGGATAACCGGTTACCGCCATGCTTGTAGTTAATAGTAATCAATTAC	2506
Db	3100	-	3099
Qy	2507	GGGGTCAATTAGTCATAGCCATATATGGGTTCCGCTACATACTTCGCTAAATGG	2566
Db	3100	-	3112
Qy	2567	CCCGCTCTGACTGTCGCCAACGACGCCGCCATGACTCTAAATGAGGATGAG	2626
Db	3113	CGGGCTGCTTAACATATGGGGCTCAGACAGATGTTACTGAGGTGACCATATGGGG	3172
Qy	2627	TATAGGTGACAGAGATATGGGGTATATGCCGATAGAGGACATCAAGCTGGCACAT	2686
Db	3173	TGTGAATACCGCACAGATCG-	3194
Qy	2687	GGCAATGCTATCGCTTACATGAACTAAATGGCAATTAGCCATTAGTCATT	2746
Db	3195	-	3195
Qy	2747	GGTTATAGCATATACTCATATGGCTTACGCTACATGCTGATGTTATCAT	2806
Db	3196	AAGGAGAATACCGCATCGATGGCTTACGCTACATGCTGATGTTATCAT	3255
Qy	2807	AATATGTCATTTATGGCTCATGGCTCATAGGCCACGTTGACATGTTATG	2866
Db	3256	AATATGTCATTTATGGCTCATGTCACATACGCCACGTTGACATGTTATG	3315
Qy	2867	ACTAGTATTAATGATTAATACCGGGCATGGCTATGGCTATATGGAGTC	2926
Db	3316	ACTAGTATTAATGATTAATACCGGGCATGGCTATGGCTATATGGAGTC	3375
Qy	2927	CGCTTACAACTACGGTAATGGCCCTGGCTGAGGCGCAACGACCCCGCCA	2986
Db	3376	CGCTTACAACTACGGCTTAATGGCCCTGGCTGAGGCGCAACGACCCCGCCA	3435
Qy	2987	TTCAGCTCATGTCGTTCCAGTAACTGACGCCATAAGGACTTTCAATGAGT	3046
Db	3436	TTGACGTCATAATGACGTTGTCCTCATGTAACGCCATAAGGACTTTCAATGAGT	3495
Qy	3047	CAATGGGTGAGTATTACGGTAACGGCCACTGGCAGTACATCAGTGTATCATG	3106
Db	3196	CAATGGGTGAGTATTACGGTAACGGCCACTGGCAGTACATCAGTGTATCATG	3555
Qy	3107	CCAGTCGCCCTATGACCTCAATGACGTTAAATGGCCCTGGCTATGCCAG	3166
Db	3556	CCAGTACGCCCTATGACCTCAATGACGTTAAATGGCCCTGGCTATGCCAG	3615
Qy	3167	TACATGCTTACGGGACTTCTACTTGCGTACTCTAGTATGATCCTATT	3226
Db	3616	TAGTACCTTATGGGACTTCTACTTGCGTACTCTAGTATGATCCTATT	3675
Qy	3227	ACCATGGTACCGGTTGGGAGTACCAATGGGCTGATAGGGTTGACTCCGG	3286
Db	3676	ACCATGGTACCGGTTGGGAGTACCAATGGGCTGATAGGGTTGACTCCGG	3735
Qy	3287	GAATTCAGTCTCCACCCCATGAGTCATAGGCTAATGGGGTTTGGCACCATAA	3346
Db	3736	GAATTCAGTCTCCACCCCATGAGTCATAGGCTAATGGGGTTTGGCACCATAA	3795
Qy	3347	CGGACTTCCAAATCTGTTAAACCCGCCCGTGGCAATGGGGTAGCGT	3406
Db	3796	CGGACTTCCAAATCTGTTACACTCCGCCATTGAGCAATGGGGTAGCGT	3855
Qy	3407	GTACGGGGAGGCTCTATAAGCAGGCTGTTAGTGACCGCTGAGTCAGCCTGGAGA	3466
Db	3856	GTACGGGGAGGCTCTATAAGCAGGCTGAGTCAGCCTGGAGTCAGCCTGGAGA	3915
Qy	3467	CGCCATCACGGTGTGTTGACTCCATAGAAGACACGGGACGATCAGCTCGGGC	3526
Db	3916	CGCCATCACGGTGTGTTGACTCCATAGAAGACACGGGACGATCAGCTCGGGC	3975
Qy	3527	CGGGAACTGTCGTTGACGGGATTCCCTGCGCAAGAGACACGGGACGATCAGCTCGGGC	3586
Db	3976	CGGGAACTGTCGTTGACGGGATTCCCTGCGCAAGAGACACGGGACGATCAGCTCGGGC	4035
Qy	3587	AGACTCTATGGCACACCCCTTGCGCTTATGCTGCTACTGTTGACTCTGGGC	3646
Db	4036	AGACTCTATGGCACACCCCTTGCGCTTATGCTGCTACTGTTGACTCTGGGC	4095
Qy	3647	CTATACCCCCGCTTCTATGCTATAGGCTAGGATGTTAGCTTAGGCTATAGGTTGG	3706
Db	4096	CTATACCCCCGCTTCTATGCTATAGGCTAGGATGTTAGCTTAGGCTATAGGTTGG	4155
Qy	3707	TTATGACCATATGGCACTCCCTATGGCTATAGGCTAGGATGTTAGCTTAGGCTATAGGTTGG	3766
Db	4156	TTATGACCATATGGCACTCCCTATGGCTATAGGCTAGGATGTTAGCTTAGGCTATAGGTTGG	4215
Qy	3767	ACATGGCTTGGCACACTATCTCTTGGCTATGGCTATCTGCTCTGGAG	3826
Db	4216	ACATGGCTTGGCACACTATCTCTTGGCTATGGCTATCTGCTCTGGAG	4275
Qy	3827	ACTGACGGACTCTGTTACGGATTTACGGATGGGCTCATTATATTAATGACATTCATA	3886
Db	4276	ACTGACGGACTCTGTTACGGATGGGCTCATTATTAATGACATTCATA	4335
Qy	3887	TATACACAAACSCCGTCCTGGCGCAGTTTATTAACATAGCTGGATCTCCA	3946
Db	4336	TATACACAAACSCCGTCCTGGCGCAGTTTATTAACATAGCTGGATCTCCA	4395
Qy	3947	CGCAACTCGCTTGGCTCCTGGAGCTGGCTCTCGGTAGGGCTGGAGCTCCA	4006
Db	4396	CGCAACTCGCTTGGCTCCTGGAGCTGGCTCTCGGTAGGGCTGGAGCTCCA	4455
Qy	4007	CATCGGACCCCTGGCTCCTGGAGCTGGCTCTGGCTGGAGCTCTGGCT	4066
Db	4456	CATCGGACCCCTGGCTCCTGGAGCTGGCTCTGGCTGGAGCTCTGGCT	4515
Qy	4067	TAACAGTGGAGGCCAGGCTTAGGCAACGACATGCCCCACAGTGGCCGACA	4126
Db	4516	TAACAGTGGAGGCCAGGCTTAGGCAACGACATGCCCCACAGTGGCCGACA	4575

QY	1547	CCCCACCCCCAAAGTCGGGTGAGGGCCAGGCGCTGGAGCCACAGTCGGGGCGCAGGC	1606	Db	2798	-----	2797
QY	1607	CCTGCCATAGCCTCGGGTTACTCATATAACTTGTGTTAACTCTTAACTCTTAACTTAA	1666	Db	2798	-----	3195
QY	1667	TTTAAAGATCTAGGAGAATCTGTTTGATTAATCTCATGACAAATCCCTTAACGT	1726	QY	1667	TTTAAAGATCTAGGAGAATCTGTTTGATTAATCTCATGACAAATCCCTTAACGT	1726
QY	1727	GAGTTTCGTTCACTGAGGCTAGGACCGTAGAGAAGATCAAGGATCTCTTGAGAT	1786	QY	1727	GAGTTTCGTTCACTGAGGCTAGGACCGTAGAGAAGATCAAGGATCTCTTGAGAT	1786
QY	2885	GCACATT-----	2891	QY	2885	GCACATT-----	2891
QY	1787	CTCTTTTCTGGGGTAATCTGCTGCTGCAAAACAAAACCCGCTACCGGGG	1846	Db	2829	CATGAGCGGATACATATTGAACTATTGAAKA--ATAAACAAATAGGGGTCCGC	2884
QY	2892	-----TCCCGAAAGTGCACCTGAGCTTAAGAACGATCAAGGATCTCTTGAGAT	2935	QY	2892	-----TCCCGAAAGTGCACCTGAGCTTAAGAACGATCAAGGATCTCTTGAGAT	2935
QY	1907	GCGAGATAACAAATACTGTCTCTTAGTGTAGCCGAGCTTCAAGAGAC	1966	QY	1907	GCGAGATAACAAATACTGTCTCTTAGTGTAGCCGAGCTTCAAGAGAC	1966
Db	2936	-----	2935	QY	2936	-----	2935
QY	1967	TCTCTAGACCGCTACATACCTCGCTCTGCTAATCTGTTACCGTGGCTGCCAGT	2026	Db	2970	GCCTTCTCGTCT-----	2982
QY	2936	-----TGACATTAACTATAAATAGGGTATAACGCGAC	2969	QY	2936	-----TGACATTAACTATAAATAGGGTATAACGCGAC	2969
QY	2027	GGCGATAACTCTACACGGGTGACTCAAGACGATAGTTACCGATAACGGGAG	2086	QY	2027	GGCGATAACTCTACACGGGTGACTCAAGACGATAGTTACCGATAACGGGAG	2086
Db	2970	-----	2982	QY	2970	-----	2982
QY	2087	CGGCGGGGTGAACGGGGGGTCTGGCACACAGCCAGTTGGAGGAAAGACCTACACC	2146	QY	2087	CGGCGGGGTGAACGGGGGGTCTGGCACACAGCCAGTTGGAGGAAAGACCTACACC	2146
Db	2993	-----	2982	QY	2993	-----	2982
QY	2147	GAACTGAGATACTCTACACGGGTGACTGAGCTATGAAAGGCCACGCTTCCCAGAAG	2206	QY	2147	GAACTGAGATACTCTACACGGGTGACTGAGCTATGAAAGGCCACGCTTCCCAGAAG	2206
Db	2983	-----CGGGCGTTCTGGGTGATGAGCGTGAACAGCTCTGACAGTCAGCTCCGGAGAC	3036	QY	2207	GGCGCAGGATATCCGTAAGGGCGGGTGGAAACAGGAGGCGCACGGAGCTCCA	2266
QY	3037	GGTCACAGCTGTCTGTAAGCGGGATGGCGGAGAGAGAGCGCTCAGGGCTCAG	3095	Db	3037	GGTCACAGCTGTCTGTAAGCGGGATGGCGGAGAGAGAGCGCTCAGGGCTCAG	3095
QY	2267	GGGGAAACGCTGTTATCTTATAGTCCCTGTCGGTTGGCAACCTCTGACTTGAGCGT	2326	QY	2267	GGGGAAACGCTGTTATCTTATAGTCCCTGTCGGTTGGCAACCTCTGACTTGAGCGT	2326
Db	3096	CGGG-----	3099	QY	3096	CGGG-----	3099
QY	2327	CGAATTTCGATGCTCGTAGGGGGGGAGCCPATGAAAAGCCAGAACGGGG	2386	Db	3100	-----	3099
Db	3100	-----	3099	QY	3100	-----	3099
QY	2387	TTTTACGGTTCTGGCTTGTGTCACATGTTCTGCGTATCC	2446	Db	3100	-----	3099
Db	3100	-----	3099	QY	3100	-----	3099
QY	2447	CCTGATTCGTTGATTAACCGTATPACCGCATGCTTGTGTTAGTTATGATGATTAC	2506	Db	3100	-----	3099
Db	3100	-----	3099	QY	3100	-----	3099
QY	2567	CCCGCTGGTGAACGGCCACAGACCCCCCGCATGACCTCAATATGAGGAGCTGA	2626	Db	3113	CCGGCTGGTGAACGGCCACAGACCCCCCGCATGACCTCAATATGAGGAGCTGA	2626
QY	3587	AGACTCTATAGCAGACCCCTTGCGCTTATGCGTATAGCTGTTGCTGGGC	3645	Db	3113	CCGGCTGGTGAACGGCCACAGACCCCCCGCATGACCTCAATATGAGGAGCTGA	2626
QY	4036	AGACTCTATAGCAGACCCCTTGCGCTTATGCGTATAGCTGTTGCTGGGC	4095	Db	3100	-----	3112
QY	3647	CTATACACCCCGCTCCCTATGCGTATAGCTGTTGCTGGGC	3705	Db	3100	-----	3112
QY	4096	CTATACACCCCGCTCCCTATGCGTATAGCTGTTGCTGGGC	4155	Db	3100	-----	3112
QY	3707	TATGGACCATATGACCACTCCCTATGCGTACGCTTCCATRACTAATCCATA	3766	Db	3100	-----	3112

Db	4156	TTATGGACCTTATGGACCTCTCCCTATGGACATTTTCATTACTAATCCATA	4215	QY	287	GGGGGGGGGGGGCTGAGGCTGCGCTGAGGCTGCGCTGAGAAGAAGAGAGTGCTGACTCATACCAAGCC	346
QY	3767	ACATGGCTCTTGCACAACTATCCTATGGCTATGGCAAACTCTGCTCAGAG	3826	Db	1562	GGGGGGGGGGGGCTGAGGCTGCGCTGAGGCTGCGCTGAGAAGAAGAGAGTGCTGACTCATACCAAGCC	1621
Db	4216	ACATGGCTCTTGCACAACTATCCTATGGCTATGGCAAACTCTGCTCAGAG	4275	QY	347	TGATGCCCATCATCCAGCCAGAAAGTGAGGGAGCACGGTGATGAGAGCTTGTG	406
QY	3827	ACTGACACGGACTCTGATTTCAGGATGGGGTCCATTATTATTAACAAATTCA	3886	Db	1622	TGAATGCCCATCATCCAGCCAGAAAGTGAGGGAGCACGGTGATGAGAGCTTGTG	1681
Db	4276	ACTGACACGGACTCTGATTTCAGGATGGGGTCCATTATTATTAACAAATTCA	4335	QY	407	TAGTGACAGTGGTGAATTGACCTTGCTTGGGATTCATTAACAAATTCA	466
QY	3887	TATACACAAAGCCCTCCCGTACCCGGTTTATTAACAAATTCA	3946	Db	1682	TAGTGACAGTGGTGAATTGACCTTGCTTGGGATTCATTAACAAATTCA	1741
Db	4336	TATACACAAAGCCCTCCCGTACCCGGTACGGGTTTATTAACAAATTCA	4395	QY	467	GGAGAGATCGTGTCTGATCACTCAGCAAAGTCGATTATTCACAAAGCC	526
QY	3947	CGCRAATCTGGGTAGCTGTTCCCGACATGGCTCTTCGGCTAGCGGGAGCTTCA	4006	Db	1742	GGAGATGGGTAATCTGATCTGATCTGCTCAACTCAGCAAAGTCGATTATTCACAAAGCC	1801
Db	4396	CGCGAATCTGGGTAGCTGTTCCCGACATGGCTCTTCGGCTAGCGGGAGCTTCA	4455	QY	527	CGTCCCGTCAACTCAGCTTAATCTCTCCAGTCAGGTTGAGCTTCCTGTC	586
QY	4007	CATCGAGCCCTGGTCCATGCCCTCAGGGCTCATGGCTCTGGCTCGGAGCTCTGTC	4066	Db	1802	CGTCCCGTCAACTCAGCTTAATCTCTCCAGTCAGGTTGAGCTTCCTGTC	1861
Db	4456	CATCGAGCCCTGGTCCATGCCCTCAGGGCTCATGGCTCTGGCTAGCGGGAGCTTCA	4515	QY	587	AGAAAACTCATCGACCAATGCCACACCAACCGAGTCGACA	646
QY	4067	TAACAGTGGGGCCAGACTAGGCACAGCAATGCCACACCAACCGAGTCGACA	4126	Db	1862	AGAAAACTCATCGACCAATGCCACACCAACCGAGTCGACA	1921
Db	4516	TAACAGTGGGGCCAGACTAGGCACAGCAATGCCACACCAACCGAGTCGACA	4575	QY	647	CATATTTGAAAGCCCTTGATGAAGAGATACTCCAGGAGCTTCATA	706
QY	4127	AGCGCGTGGGGTAGGTATGTCGTGAATAATGAGCTGGCTGGACCGTG	4186	Db	1922	CATATTGAAAGCCCTTGATGAAGAGATACTCCAGGAGCTTCATA	1981
Db	4576	AGCGCGTGGGGTAGGTATGTCGTGAATAATGAGCTGGCTGGACCGTG	4635	QY	707	GGATGGAGATCTGGTATCGTCTCGATTCAGGTTAATGAACTGCAATTATCA	766
QY	4187	ACCGAGATGGAGACTTAAGCAGGGCAAGAGATACTCCCGTCTGAGTGTG	4246	Db	1982	GGATGGAGATCTGGTATCGTCTCGATTCAGGTTAATGAACTGCAATTAC	2041
Db	4636	ACCGAGATGGAGACTTAAGCAGGGCAAGAGATACTCCCGTCTGAGTGTG	4695	QY	767	TTATTTCCTGTCATAAAATTAAGGTATCAAGTGAAGAATTCACCTGAGCTTCATA	826
QY	4247	TCTGATAAGGTAGGTAATCTCGTCTGAGCTTCAGGTTAACCGTGGAGCTG	4306	Db	2042	TTATTTCCTGTCATAAAATTAAGGTATCAAGTGAAGAATTCACCTGAGCTTCATA	2101
Db	4696	TCTGATAAGGTAGGTAATCTCGTCTGAGCTTCAGGTTAACCGTGGAGCTG	4755	QY	827	AATCGCGTGGAGATGGCAGAACTTCAGGTTTCCAGCTTGTCACATCAACTA	886
QY	4307	TCTGAGCAGTACTGTTCCATGGGCTCTCTGGAGTCACCGTCACG	4366	Db	2102	AATCCGGTCAAGATGGCAGAACTTCAGGTTTCCAGCTTGTCACAGGTCACG	2161
Db	4756	TCTGAGCAGTACTGTTCCATGGGCTCTCTGGAGTCACCGTCACG	4815	QY	887	CATAGCTGTCATCAAATCTCGATCCGATCAGGAACTTATTCAGGATCG	946
QY	4367	GACTGTTCTTCACATGGGCTCTCTGGAGTCACCGTCACG	4409	Db	2162	CATAGCTGTCATCAAATCTCGATCCGATCAGGAACTTATTCAGGATCG	2221
Db	4816	GACTGTTCTTCACATGGGCTCTCTGGAGTCACCGTCACG	4858	QY	947	CTGAGGAGACGAAATACCGATCGCTGTTAAAGGCAATACAAACGGATCCAA	1006
RESULT 15							
AXT138936	LOCUS	AX138936	DEFINITION	5111 bp	DNA	LINEAR	PAT 30-MAY-2001
ACCESSION	AX138936	VERSION	5	from Patent	EP1052286.		
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE							
AUTHORS	Morsev, M.A. and Sheppard, M.G.	TITLE	Human growth hormone releasing hormone compositions	PATENT	EP 1052286		
JOURNAL	Patent: EP 1052286-A 55 15-NOV-2000;	PATENT	Pfizer Products Inc. (US)	LOCATION	Location/Qualifiers		
FEATURES	1. -511	source	/organism="synthetic construct"	/mol-type="unassigned DNA"	/ab_xref="Taxon:32630"	/note="PGRHR1-29y1a1522CMV construct"	
ORIGIN							
Query	Best Local Similarity	31.3 %;	Score	2008.6;	DB	6;	Length 5111;
Matches	3058;	Conservative	0;	Mismatches	239;	Indels	826;
					Gaps	8;	

QY	1367 TCGAGCAAGACGTTCCCGTGAATANGCTATAACCCCCCTGTTAACCTTGTATTACGTTRGT	Db	3100 -----	3099
Db	2642 TCGAGCAAGACGTTCCCGTGAATANGCTATAACCCCCCTGTTAACCTTGTATTACGTTRGT	QY	2007 GGGTCATTAGTCATAGGCCATATATGGACITCCCGTTACATAACTTACGGTAATGG	2566
QY	1427 AACAGACAGTTTATGTTCATGATGATAATTATTTATCTGTGAATGTCATGTAACAGA	Db	3100 -----	TGTTGGCGGGTGT 3112
Db	2702 AACAGACAGTTTATGTTCATGATGATAATTATTTATCTGTGAATGTCATGTAACAGA	QY	2567 CCGCCTGGCTGACGCCAACGACCCGCCCATCGTCATAATGACGAGATCTGA	2626
QY	1487 GATTGAGAACAACGTTCCCGTGAATGTCATGATGATAATTATTTATCTGTGAATGTCATGTAACAGA	Db	3113 CGGGCTGGCTTAATCTGCGCATCTGAGGAGATGTACTGAGAGATGTCACCATGCGG	3172
Db	2762 GATTGAGAACAACGTTCCCGTGAATGTCATGATGATAATTATTTATCTGTGAATGTCATGTAACAGA	QY	2427 TATAGGTGACAGACGATAATGAGGCTTATATCGCGATAGAGGACAGTCAGTCAGTCAG	2686
QY	1547 CCCACACCCCAAGTCGGTGAGGCCAGGCTCGCAGAACGTCGGGGAGGAGG	Db	3173 TGTGAATACCCACAGATGCC	3194
Db	2798 -----	QY	2087 GCCAAATGCAATATGATCAATATGGCAATTAGCCATTAGTCATT	2746
QY	1607 CCTGCCATAGCCTCAGGTTACCTATATACCTTGTAGTTAAACCTCATTTAA	Db	3195 -----	T 3195
Db	2798 -----	QY	2798 ATTATGAGCATTTATCGGGTTATGCT	2828
QY	1567 TTAAAGGATCTAGGTCAGATCCTTTGATTAATCTCATGCCAAATCCCTTAACGT	Db	3196 AAGGAGAAATCCGCTCAGATGGCTATTGGCATATGCTATACGTTGATCAT	3255
Db	2829 CATGAGCGGATACATATTGATGTTAGAAGA-----ATAACAAATAGGGGTCCGC	QY	2007 AATATGACATTATATGGCTCATGTCATAATGCCATAATGCCGCAATGTCATGATTG	2866
QY	1727 GACTTGTGTCGACTGAGGCTAGACCCCTAGAAAAGATCAAGAGTCCTGTGAGAT	Db	3256 AATATGACATTATATGGCTCATGTCATAATGCCATAATGCCGCAATGTCATGATTG	3315
Db	2885 GCACATT-----	QY	2067 ACTAGTATTAATAGTATCATATTAGGGCATTTGTCATAGCCATAATGCCGCAATGTCATGATTG	2926
QY	1787 CCTTTTCTGGCGTAATCTGCTGTCGAAACAAACACCCCTACAGCGGTG	Db	3116 ACTAGTATTAATAGTATCATATTAGGGCATTTGTCATAGCCATAATGCCGCAATGTCATGATTG	3375
Db	2892 -----	QY	2227 CGGTACATAACTTACGGTAATGGCCGACTGGTACGCCAACGACCCGCCA	2986
QY	1847 GTTGTTGCCGATCAAGAGCTACCAACTCTTTCGGAGGTAATCGCTCAGCGA	Db	3176 CGGTTACATAACTTACGGTAATGGCCGCTGGTACGCCAACGACCCGCCA	3435
Db	2936 -----	QY	2987 TTAGCGTATGAGGTAATTCGCAATGTAACGCCAATAGGGGATTCGATGAGT	3046
QY	1907 GCGCAGATAACCAAATACGTCTCTACCGTGTAGTAGCCACACTTCAGAC	Db	3436 TTGACGTCATAATGAGTGTCTGAGTCAGAACCAATAGGGACTTCAGT	3495
Db	2936 -----	QY	3047 CAACTGGTGGAGTATTAGGTAACCTGCCACTTGGCGTACATGTCATGAT	3106
QY	1967 TCTGTAGCACGCCATACATCTGCTCTCTAACTCTGTTACAGTGGCTGCGCAT	Db	3496 CAACTGGTGGAGTATTAGGTAACCTGCCACTTGGCGTACATGTCATGAT	3555
Db	2936 -----	QY	3107 CCAAGTCGCCCTATGACTCAATGACGCTAATGGCGCCNGCGATATGCCAG	3166
QY	2027 GGCATAATGCTGCTCTACCGGGTGGACTCAGACGATGTTACCGATAAGGCGAG	Db	3556 CCAGTACGCCCTATGACTCAATGACGCTAATGGCGCCNGCGATATGCCAG	3615
Db	2970 GGCCTTCTGCTCT-----	QY	3167 TACATGACCTTACGGGACTTCTACTGGTGTACCTCTAGTATGATGATT	3226
QY	2087 CGGCGGCTGAACTGGGGTGTGCAACAGCCACGCTTGAGGAGACGACCTACCC	Db	3616 TACATGACCTTACGGGACTTCTACTGGTGTACCTCTAGTATGATGATT	3675
Db	2983 -----	QY	3227 ACCATGCGTACGGTTTGCGAGTACCAATGGGGTGTAGCGTTGACTCGGG	3286
QY	2147 GAACTGAGATACCTACAGGGTACGCTATGAGAACGCCAACGTTCCGAGGGAGA	Db	3676 ACCATGCGTACGGGTTTGCGAGTACCAATGGGGTGTAGCGTTGACTCGGG	3735
Db	2983 -----	QY	3287 GATTCGAGCTCCGCCATGAGCTCATGGGGTTTGGCACCACCTCAA	3346
QY	2207 GCGCAGACGTTATCGGTAGGGAGGGTGGAGACAGGAGGCCAACGGAGCTCCA	Db	3736 GGTTCGAGCTCCACCCCATGAGCTCATGGGGTGTAGCGTTGACCAACCTCAA	3795
Db	3037 GGTCAACAGCTGCTGTAAGGGGATGCGGGAGGAGCAACGCCGTCAGGGGGCTAG	QY	3347 CGGGACTTCCAAATGTTGTTATACCCGGCCGTGACCAATGGGGTAGCGGT	3406
QY	2267 GGGGAAACGCCCTGTTAGCTCTGCGACCTCTGACTTGAGCT	Db	3736 CGGGACTTCCAAATGTTGAGCTACACTCCGCCATGAGCTCATGGGGTGTAGCGGT	3855
Db	3096 CGGG-----	QY	3407 GTRACGGTGGAGGCTCTATAGCAGGCTCTTGTGACCGTCACTGTCAGTCAGTCAG	3466
QY	2327 CGATTGAGTCTGCTCAGGGGGGGAGGCTATGAGAACGCCAACGCCAACGCC	Db	3856 GTRACGGTGGAGGCTCTATAGCAGGCTCTGAGCTGAGCTGAGCTGAGCTGAG	3915
Db	3100 -----	QY	3467 CGGCATCACCGCTTGTGACTCCATAGAACACCGGGACGATCAGCTCCGCGC	3526
QY	2387 TTTCAGGTCTGGCCCTTGTGCTGCTCAAGTCTTCTGGGTATCC	Db	3916 CGGCATCACCGCTTGTGACTCCATAGAACACCGGGACGATCAGCTCCGCGC	3975
Db	3100 -----	QY	3527 CGGAAACGGTCACTGGAGGGATTCCCGTGCAGAGTGCAGCTGAGCTGCGGT	3586
QY	2447 CCTGATTCTGATAACCGGATTACCGCCATCATGAGTAAATGAACTCAATTAC	Db	3527 CGGAAACGGTCACTGGAGGGATTCCCGTGCAGAGTGCAGCTGAGCTGCGGT	3586

Db	3976	CGGGACGGTGCAATTGAAAGCGGATTCGGTCCAAAGTGACGTAAAGTACCGCTAT	4035
QY	3587	AGACTCTATGGCACACCCCTTGGCTCTATGCGCTATACTGTTTGCTTGGGC	3646
Db	4036	AGACCTATGGCACACCCCTTGGCTCTATGCGCTATACTGTTTGCTTGGGC	4095
QY	3647	CTATACCCCGCTCCCTATGCTATGGTAGGTAGGTGTTGGCT	3706
Db	4096	CTATACCCCGCTCCCTATGCTATGGTAGGTAGGTGTTGGCT	4155
QY	3707	TTATGACCTTATGACCACTCCCTATGGCTATGCCAAACTCTGCTCTAGCTAGGCTAATGGCT	3766
Db	4156	TTATGACCTTATGACCACTCCCTATGGCTATGCCAAACTCTGCTCTAGCTAGGCTAATGGCT	4215
QY	3767	ACATGGCTTGGCACACCTATCTATGGCTATGCCAAACTCTGCTCTAGCTAGGCTAATGGCT	3826
Db	4216	ACATGGCTTGGCACACCTATCTATGGCTATGCCAAACTCTGCTCTAGCTAGGCTAATGGCT	4275
QY	3827	ACTGACCGACTCTGTTACAGGATGGGTCATTTATTAACATAGGGATCTCA	3886
Db	4276	ACTGACCGACTCTGTTACAGGATGGGTCATTTATTAACATAGGGATCTCA	4335
QY	3887	TATACAACACAGGCCCTCCCGCTGCCGAGTTTATTAACATAGGGATCTCA	3946
Db	4336	TATACAACACAGGCCCTCCCGCTGCCGAGTTTATTAACATAGGGATCTCA	4395
QY	3947	CGCGAATCTGGGAGCTGTTCCGGACATGGCTTCTCCGGTAGGGGACCTCA	4006
Db	4396	CGCGAATCTGGGAGCTGTTCCGGACATGGCTTCTCCGGTAGGGGACCTCA	4455
QY	4067	TAACATGGGGGAGACTTGGGACAGCAATGCCGCCACACCACTGGTGCAGCA	4126
Db	4456	TAACATGGGGGAGACTTGGGACAGCAATGCCGCCACACCACTGGTGCAGCA	4515
QY	4007	CATCGAGCCCTGGTCCATGGCTCCAGGGCTCATGGTGCCTCGAGCTCTGTC	4066
Db	4516	CATCGAGCCCTGGTCCATGGCTCCAGGGCTCATGGTGCCTCGAGCTCTGTC	4575
QY	4127	AGGCCTGGGGTAGGGTATGCTGAAATGAGCTGGAGTTGGCTCGACCGCTG	4186
Db	4576	AGGCCTGGGGTAGGGTATGCTGAAATGAGCTGGAGTTGGCTCGACCGCTG	4635
QY	4187	ACGGAGATGGGAGACTTAAAGGAGAGAGATGGAGCTGGTGTGTTGAT	4246
Db	4636	ACGGAGATGGGAGACTTAAAGGAGAGAGATGGAGCTGGTGTGTTGAT	4695
QY	4247	TCTGATAAGCTGGAGAGGTAACCTGGTGTGGGGCTGTTAACGGTGTGAG	4306
Db	4696	TCTGATAAGCTGGAGAGGTAACCTGGTGTGGGGCTGTTAACGGTGTGAG	4755
QY	4307	TCTGAGGAGAGACTCTGGGCGGGGACAGACATAATAGCTGACAGCTAAC	4366
Db	4756	TCTGAGGAGAGACTCTGGGCGGGGACAGACATAATAGCTGACAGCTAAC	4815
QY	4367	GACTGTTCCCTCCATGGGCTTCTGCAGTCGGTACCGTCAACG 4409	
Db	4816	GACTGTTCCCTCCATGGGCTTCTGCAGTCGGTACCGTCAACG 4858	

Search completed: October 13, 2004, 01:30:16

Job time : 24056 SECs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using Bw model
Run on: October 12, 2004, 14:01:32 ; Search time 14701 seconds
(without alignments)

130316.588 Million cell updates/sec

Title: US-09-996-128a-1
Perfect score: 6408
Sequence: 1 attccgcagatccgcac.....tctttttaaaaacccga 6408

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : EST:*

1: em_estba:*

2: em_eathum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_eston:*

17: em_gss_hum:*

18: em_gss_ivv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_dhg:*

27: em_gss_vti:*

28: gb_gss1:*

29: gb_gss2:*

ALIGNMENTS

RESULT 1
AK014619
LOCUS AK014619 1932 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4633402C07 product:tyrosinase, full insert sequence.
ACCESSION AK014619
VERSION AK014619.1 GI:12852585
KEYWORDS HCC; CRP; trapper
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 Carnici, P. and Hayashizaki, Y.
AUTHORS Carnici, P. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 9927953
PUBMED 10349636
REFERENCE 2 Carnici, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499574
PUBMED 11042159
REFERENCE 3 BM557397
PUBMED 10349636

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1180.4	18.4	1932 11 AK014619	AK014619 Mus muscu
2	885.8	13.8	1063 12 BM463960	BM463960 AGENCOURT
3	874.6	13.6	9017 BM190117	BM190117 AGENCOURT
4	849.4	13.3	1068 12 BM557397	BM557397 AGENCOURT

		VERSION	BM463960.1 GI:18513002
		KEYWORDS	EST.
		SOURCE	Homo sapiens (human)
		ORGANISM	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
		REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; (bases 1 to 1063)
	AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/
	TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
	JOURNAL	Contact: Robert Strausberg, Ph.D.	Email: cgs@nih.gov
	COMMENT	Found through the I.M.A.G.E. Consortium/LINL at: http://image.lnl.gov	Tissue Procurement: ARCC/DCB/DTB
Db	755	GGAAACAGAAATTGGAAACTAACITGGGATGAGAACTTCACTTCATACGGATG	814
Qy	5229	GCGGATGGAAAGTGTACATTGCAAGATGAGTCAATGGAGGTAGGACCCAC	5288
Db	815	GAGAGATGRRGAAACTGTGCAATTGAGATGAGTCTTGGAGATGAGGACCCAC	874
Qy	5289	AAATCTTAACCTACTACGCCAGCATTCATCTCTGGAGATGTCCTAGCG	5348
Db	875	AATCTTAACCTACTACGCCAGCATTCATCTCTGGAGATGTCCTAGCG	934
Qy	5349	ATGGAGGAGTACACAGCCATCAGCTTATGATGAACTGAACTGAGCTT	5408
Db	935	ATCAGAGAGTAACTAGCCATCAGTTATGGATGAACTGAACTGAGCTT	994
Db	5409	GCGTAACTCTGGAAACATGCAAACTCAGGACCCAAAGCTCCCTCTCAG	5468
Qy	995	ACGTAATCCGGAAACATGCAAACTCAGGACCCAGCTCCATCTCAGAGCT	1054
Qy	5469	AGAATTGCTGACTTGTGAGTTGACCTGATGAACTGAACTGAGCTT	5528
Db	1055	GAATTTGCTGACTTGTGAGTTGACCTGATGAACTGAACTGAGCTT	1114
Qy	5529	CAGCTTGTAACTACTGGAGATTGCTACTACTGGATGAGCTGAGCTGAGCT	5588
Db	1115	CAGCTTGTAAACACTGGAGGTTGCACTACAGGATGAGCTTC	1174
Qy	5589	TCAAGCAGGATGCAACGCTTGTGAGCTTGTGAGCTTGTGAGCTTGTGAGCT	5648
Db	1175	TCAAGTGTGCAACGATCCCATTCTCTCACCAGTGTGAGCTTGTGAGCT	1234
Qy	5649	GGGATCTGCAACGATCTCTCTCACCAGTGTGAGCTTGTGAGCTTGTGAGCT	5708
Db	1235	GGGATCGGCAACGATCCCATTCTCTCACCAGTGTGAGCTTGTGAGCT	1294
Qy	5709	GCAGTGGCTCGGAAGCAGCTCCCTCTCAAGAAGTTTACCCAGAAGCTGAGCT	5768
Db	1295	ACAAATGGCTGGAAGCAGCCCTCTTGGAGTTACCCAGAAGCTGAGCT	1354
Db	5769	TGAATGAAACGGAACTCTACGGTCTTAACTCTGTACAGAAATGGTATT	5828
Qy	1355	CGGGATAACAGAGCTTCTACATGGTCTTCAACCCCTATAGAATGGTATT	1414
Qy	5829	CTTAAATTCCTCAAAAGATGTGGATAGTCAAGATTCAGCCAA	5888
Db	1415	CTCTATAACATCCAAAGGATCTGGATATGACTACGCTACCTCCAGAGTCAGTCAGG	1474
Qy	5889	CTCTTTCAAGACTCATTTAGTCTTATGGTAACTGAGCTGAGCTGAGCT	5948
Db	1475	CTTGTACAGAAATTATGGCTACTTGTGAACTGAGCTGAGCTGAGCT	1534
Qy	5949	CCTGGGGCGCGGATGTGGCTCTACTGCTCTGGAGGGTTGTGAGCT	6008
Db	1535	TCTGGGGCGGACTGTGGCTGAGCTGAGCTGAGCTGAGCTGAGCT	1554
Qy	6009	GCTGTTGCTGCTCTTGTGAGCTGAGCTGAGCTGAGCTGAGCT	6059
Db	1595	GCTATGCTCTGAGAGGAGAGGAGGAGGAGGAGGAGGAGCTCT	1654
Qy	6060	CATGCGAAAGAGGATTACCAAGT---TGTATCAGAGGCAATTATAAAGGCTT	6116
Db	1655	CATGGCAAAAGACGACTTACCAAGCTGCTGAGCTGAGCTGAGCT	1714
Qy	6117	ATAGAGTAGGCCAAAGGCTGACCTACTCTACT	6154
Db	1715	AAACAGTGGGACTGAGGGTTTACCTCTCTGAGCT	1752
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		/lab_host="DH10B (phage-resistant)"	
		/clone_lib="NIH MGC-72"	
		/note="Organ: skin; Vector: pCMV-SPORT6; Site:1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo: dr. Average insert size 2 kb. Library constructed by Life Technologies."	
		Query Match	ORIGIN
		Best Local Similarity	13.8%
		Score	885.8
		DB	12
		Length	1063
		Matches	937
		Conservative	0
		Mismatches	33
		Indels	5
		Gaps	3
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Db	94	TGTGAGCTAGAGGAGATGCTCTGCTGCTGAGTTTCA	153
Qy	4557	GACCTCGTGGCATTTCCTAGGCTGTGCTCTCTAAGACCTGATGGAGAGA	4616
Db	154	GACCTCGTGGCATTTCCTAGGCTGTGCTCTCTAAGACCTGATGGAGAGA	213
Qy	4617	ATGCTGTCACCGTGGAGCGGGACAGAGTCTGCTGAGCTGAGCTGTC	4676
Db	214	ATGCTGTCACCGTGGAGCGGGACAGAGTCTGCTGAGCTGAGCTGTC	273
Qy	4677	CTGTCAGAAATTCTCTGTCTCAATGCAACCTTGTGGCTCAATTCTTCAGAGG	4736
Db	274	CTGTCAGAAATTCTCTGTCTCAAGGCTTCTGAGGAGCTGAGCTGTC	333
Qy	4737	GGATGCCGGAGTGTGGCTTCGCTTATAAGGACTGCACTGCTGCTGCA	4796
Db	334	GGATGCCGGAGTGTGGCTTCGCTTATAAGGACTGCACTGCTGCTGCA	393
Qy	4797	CTTCATGGGATTCACTGTGGAAACTGCAAGTTGCTTGGGACCAACTGCAGA	4856
Db	394	CTTCATGGGATTCACTGTGGAAACTGCAAGTTGCTTGGGACCAACTGCAGA	453
Qy	4857	GAGAGCACTTGTGGAGGAGAAACTCTGAGTTGAGTGTGGCCAGAGGAAATT	4916
Db	454	GAGAGCACTTGTGGAGGAGAAACTCTGAGTTGAGTGTGGCCAGAGGAAATT	513
Qy	4917	TTCGCTACTCTTGTGAAAGCATCATGCTGAGCTATGCCATAGG	4976
Db	514	TTTGCTACTCTTGTGAAAGCATCATGCTGAGCTATGCCATAGG	573
Qy	4977	GACCTATGGCAAATGAAATGGTAAACACCATGTTAACGACATCAATTATGCA	5036

RESULT 2

BM463960 LOCUS ABNCOURT DEPOSITION 5', mRNA Sequence. ACCESSION BM463960

1063 bp

linear

EST 05-FEB-2002

IMAGE:553977

Db 574 GACCTATGCCAATGAAATGGTCAACACCATGTTAACGACATCATATTAGA 633
 QY 5037 CCTCTTGCTGGATGCAATTATATGTCGCAATGGATGACTGCTGGGGATATGAAT 5096
 Db 634 CCTCTTGCTGGATGCAATTATGTCGCAATGGATGACTGCTGGGGATATGAAT 693

QY 5097 CTGGAGAGCATGGATTGCCATGAGACCAAGCTTCTGCCTGGATGACTCT 5156

Db 694 CTGGAGAGCATGGATTGCCATGAGACCAAGCTTCTGCCTGGATGACTCT 753

QY 5157 CTGGATGGCTGGGACACAGAAATCCAGAGCTGACAGAATGAAACTCTATGCC 5216

Db 754 CTGGATGGCTGGGACACAGAAATCCAGAGCTGACAGAATGAAACTCTATGCC 813

QY 5217 ATATGGACTGGGGATGGGAAACAGAAATCCAGAGCTGACAGAATGAAACTCTATGCC 5276

Db 814 ATATGGACTGGGGATGGGAAACAGAAATCCAGAGCTGACAGAATGAAACTCTATGCC 873

QY 5277 TCAAGACCCACAATCTACTACTCGCCAGCATGATGATCTCTCTGGAGAT 5336

Db 874 TCAAGACCCACAATCTACTACTCGCCAGCATGATGATCTCTCTGGAGAT 932

QY 5337 TGTCTGTAACGGGATGGAGAGTACACGCCATCAGTTATGCAATGAAACGCCGA 5396

Db 933 TGTCTGTAACGGGATGGAGAGTACACGCCATCAGTTATGCAATGAAACGCCGA 992

QY 5397 GGGACCTTAACTGGGAACTGAAATCCAGAACCCAGGGTCCCTC 5456

Db 993 GGGACCTTAACTGGGAACTGAAATCCAGAACCCAGGGTCCCTC 1048

QY 5457 TTCACTGATGTAGA 5471

Db 1049 TTCACTAAGGTANA 1063

RESULT 3

BU190117 BU190117 984 bp mRNA linear EST 04-SEP-2002

LOCUS BU190117 984 bp mRNA linear EST 04-SEP-2002

DEFINITION AGENCYCOURT_8076683 NIH_MGC_112 Homo sapiens cDNA clone IMAGE_6089012

ACCESSION 5' mRNA Sequence.

VERSION BU190117.1 GI:22704101

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 984) NIH-MGC <http://mgc.nci.nih.gov/>

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strauberg, Ph. D.

COMMENT Email: cgsab@remall.nih.gov

Tissue Procurement: DCTD/NCI

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILN)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILN at: <http://image.lnl.gov>

Plate: LILN2328 row: b column: 21

High quality sequence stop: 661.

FEATURES

Source

1 . 984

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/mol_type="mRNA"

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/tissue_type="melanotic melanoma, cell line"

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/note="Organ: skin; Vector: pOTB7; Site_1: Xhol; Site_2:

ORIGIN

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Best Local Similarity 96.6%; Pred. No. 4. 8e-240;

Matches 926; Conservative 0; Mismatches 29; Indels 4; Gaps 3;

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Db 64 CATTCCCTAGACQCTGTCTCTTAAGAACCTGTGAGGAAGGATGCTGCCACCG 123

Db 4630 TCGAGGGAGCAGGAGCCCTGTCAGCAAGAACCTGTGAGGAAGGATGCTGCCACCG 63

Db 124 TGGAGCAGGAGCAGGAGCCTGTCAGCAAGAACCTGTGAGGAAGGATGCTGCCACCG 183

Db 4690 CTCTGTCCTAGACQCTGTCTCTTAAGAACCTGTGAGGAAGGATGCTGCCACCG 4749

Db 184 CTCTGTCCTAGACQCTGTCTCTTAAGAACCTGTGAGGAAGGATGCTGCCACCG 243

Db 4750 TCGTGGCTTCCTCTTATATAGAACCTGCTCCAGTCGCTCTGTCAGGACCTGTGAGGAATC 4809

Db 244 TCTGGCTTCCTTATATAGAACCTGCTCCAGTCGCTCTGTCAGGACCTGTGAGGAATC 303

Db 4810 AACTGTGAACTGCAAGTGGCTTGGGACCAACTCACAGAGAGAACCTGTGAGGAATC 4869

Db 304 AACGTGCAACTGCAACTGGCTTGGGACCAACTCACAGAGAGAACCTGTGAGGAATC 363

Db 4870 GTGAGAGAACATCTGATTGAGGCCAGAGAGAACATTTCCTACTCTC 4929

Db 364 CTGGAGAACAACTCTGATTGAGGCCAGAGAGAACATTTCCTACTCTC 423

Db 4930 ACTTTAGCAAGGATACATCATCACGACTCGAGACTAGTCATCCCATGGGCAA 4989

Db 424 ACTTTAGCAAGGATACATCACGACTCGAGACTAGTCATCCCATGGGCAA 483

Db 4990 ATGAAATGGCAACCCATGTTAACGACATCATATTATGACCTCTTGTGTTGG 5049

Db 484 ATGAAATGGCAACCCATGTTAACGACATCATATTATGACCTCTTGTGTTGG 543

Db 5050 ATGCAATTATGTCATGGATCTGCTGGGGATATGAAACCTGTGAGGACATT 5109

Db 544 ATGCAATTATGTCATGGATCTGCTGGGGATATGAAACCTGTGAGGACATT 603

Db 5110 GATTGGCCATGAAGGACCAAGTTCTGCCTGGGATAGATGACTCTCTGTGCGATGG 5169

Db 604 GATTGGCCATGAAGGACCAAGTTCTGCCTGGGATAGATGACTCTCTGTGCGATGG 663

Db 5170 GAACAAAGAATCCAGAGCTGAGGGATGAAACTCACTATTCCATATTGGGACTGG 5229

Db 664 GAACAAAGAATCCAGAGCTGAGGGATGAAACTCACTATTCCATATTGGGACTGG 723

Db 5230 CGGGATGCAAGAAGTGTGACATTGACAGATGGACATGGAGGTCAGACCCACA 5289

Db 724 CGGGATGCAAGAAGTGTGACATTGACAGATGGACATGGAGGTCAGACCCACA 783

Db 5290 AATCTTAACCTACTCAACCCAGCATCTCTCTCTGGAGATGCTGTGAGGCGA 5349

Db 784 AACCTTAACCTACTCAACCCAGCATCTCTCTCTGGAGATGCTGTGAGGCGA 843

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ACCESSION	BM557397	1 (bases 1 to 903)	QY	4977	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
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ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.	1 (bases 1 to 1068)	QY	5097	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
REFERENCE	Nih-Mgc http://mgc.ncbi.nih.gov/	1 (bases 1 to 1068)	Db	645	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)	1 (bases 1 to 1068)	QY	5157	CTGTTGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
TITLE	Unpublished (1999)	1 (bases 1 to 1068)	Db	705	CTCTGGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
JOURNAL	Contact: Robert Strausberg, Ph.D.	1 (bases 1 to 1068)	QY	5217	ATATT-GGAACCTGGGGATGAGAAAGTGTGACATTTGAGATGAGTACAT-GGGA
COMMENT	Email: cgabs-r@mail.nih.gov	1 (bases 1 to 1068)	Db	765	ATATGGGGACTCTGGGATGAGAAAGTGTGACATTTGAGATGAGTACATGGGA
Tissue Procurement: ATCC/DCTP/DTP	http://image.llnl.gov	1 (bases 1 to 1068)	QY	5275	GGTCAGACCCCA-CAAACTCTAACTTACAGCTTCAGCCATCATCTCTCTGCA
cDNA Library Preparation: Life Technologies, Inc.	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (IINL)	1 (bases 1 to 1068)	Db	825	GGTCAGACCCCAACCAAACTTACAGCTTCAGCCATCATCTCTGCA
DNA Sequencing by: Agencourt Bioscience Corporation	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/IINL at:	1 (bases 1 to 1068)	QY	5334	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/IINL at:	http://image.llnl.gov	1 (bases 1 to 1068)	Db	885	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG
Plate: ILMN1255 row: n column: 11	High quality sequence stop: 643.	1 (bases 1 to 1068)	QY	5392	CCCGAGGGACCTTACCGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
FEATURES	source	1 (bases 1 to 1068)	Db	945	CCGAGGGATTTTACGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
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Query Match	Best Local Similarity 13.3%; Score 849.4; DB 12; Length 1068;	1 (bases 1 to 1068)	Db	1065	C 1065
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QY	4557	45 TGTGAGGATAGAGAGAGATGCTCTGGTACTGCGCTGCTGGAGTTCCA	4556	RESULT 5	BU183039
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QY	4617	4617 ATGTGTCACCGGGAGGGAGGGAGGGCTCTGGCTCTGGAGTTCCA	4616	DEFINITION	AGENCOURT_7932460 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6157206
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Db	225	CTGTCAGAAATCTCTCTGGCTCAATGACCACTGGGCTCAATTCCCTCACAGGGT	284	KEYWORDS	EST.
QY	4737	4737 GGATGACCGGGAGTGTGGCTCTGGCTCTGGCTCTGGCTCTGGCTCTGGCA	4796	SOURCE	Homo sapiens (human)
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QY	4797	4797 CTTCATGGGATCACTGTGGAAGTGTGGCTCTGGCTCTGGCA	4856	REFERENCE	1 (bases 1 to 903)
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			Db	525	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
			QY	5037	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			Db	585	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			QY	5097	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			Db	645	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			QY	5157	CTGTTGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			Db	705	CTCTGGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			QY	5217	ATATT-GGAACCTGGGGATGAGAAAGTGTGACATTTGAGATGAGTACAT-GGGA
			Db	765	ATATGGGGACTCTGGGATGAGAAAGTGTGACATTTGAGATGAGTACATGGGA
			QY	5275	GGTCAGACCCCA-CAAACTCTAACTTACAGCTTCAGCCATCATCTCTGCA
			Db	825	GGTCAGACCCCAACCAAACTTACAGCTTCAGCCATCATCTCTGCA
			QY	5334	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG
			Db	885	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG
			QY	5392	CCCGAGGGACCTTACCGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
			Db	945	CCGAGGGATTTTACGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
			Db	1005	CCCTCTCNCCTGAGTAATTAATTGCTGAATTGGACCAATATGAAATCGGATT
ORIGIN			QY	5508	C 5508
			Db	1065	C 1065
			QY	4497	TGGTGAATTCCGGGAGAGATGCTCTGGTACTGCGCTGCTGGAGTTCCA
			Db	105	ATGCGTCTCCGGCTGGCTCTGGCTCTGGCTCTGGAGTTCCA
			QY	4617	ATGTGTCACCGGGAGGGAGGGAGGGCTCTGGCTCTGGAGTTCCA
			Db	165	ATGCGTCTCCGGCTGGCTCTGGCTCTGGCTCTGGAGTTCCA
			QY	4677	CTGTGAGAAATCTCTCTGGCTCAATGACCACTGGGCTCAATTCCCTCACAGGGT
			Db	225	CTGTCAGAAATCTCTCTGGCTCAATGACCACTGGGCTCAATTCCCTCACAGGGT
			QY	4737	GGATGACCGGGAGTGTGGCTCTGGCTCTGGCTCTGGCA
			Db	285	GGATGACCGGGAGTGTGGCTCTGGCTCTGGCA
			QY	4797	CTTCATGGGATCACTGTGGAAGTGTGGCTCTGGCA
			QY	4917	TTTGCTCTACTTGTAGAAAGCTTACCATCAGCTCAGACTATGTCAGT
			QY	4977	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
			Db	525	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
			QY	5037	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			Db	585	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			QY	5097	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			Db	645	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			QY	5157	CTGTTGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			Db	705	CTCTGGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			QY	5217	ATATT-GGAACCTGGGGATGAGAAAGTGTGACATTTGAGATGAGTACAT-GGGA
			Db	765	ATATGGGGACTCTGGGATGAGAAAGTGTGACATTTGAGATGAGTACATGGGA
			QY	5275	GGTCAGACCCCA-CAAACTCTAACTTACAGCTTCAGCCATCATCTCTGCA
			Db	825	GGTCAGACCCCAACCAAACTTACAGCTTCAGCCATCATCTCTGCA
			QY	5334	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG
			Db	885	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG
			QY	5392	CCCGAGGGACCTTACCGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
			Db	945	CCGAGGGATTTTACGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
			Db	1005	CCCTCTCNCCTGAGTAATTAATTGCTGAATTGGACCAATATGAAATCGGATT
			QY	5508	C 5508
			Db	1065	C 1065
			QY	4497	TGGTGAATTCCGGGAGAGATGCTCTGGTACTGCGCTGCTGGAGTTCCA
			Db	105	ATGCGTCTCCGGCTGGCTCTGGCTCTGGCTCTGGAGTTCCA
			QY	4617	ATGTGTCACCGGGAGGGAGGGAGGGCTCTGGCTCTGGAGTTCCA
			Db	165	ATGCGTCTCCGGCTGGCTCTGGCTCTGGCTCTGGAGTTCCA
			QY	4677	CTGTGAGAAATCTCTCTGGCTCAATGACCACTGGGCTCAATTCCCTCACAGGGT
			Db	225	CTGTCAGAAATCTCTCTGGCTCAATGACCACTGGGCTCAATTCCCTCACAGGGT
			QY	4737	GGATGACCGGGAGTGTGGCTCTGGCTCTGGCTCTGGCA
			Db	285	GGATGACCGGGAGTGTGGCTCTGGCTCTGGCA
			QY	4797	CTTCATGGGATCACTGTGGAAGTGTGGCTCTGGCA
			QY	4917	TTTGCTCTACTTGTAGAAAGCTTACCATCAGCTCAGACTATGTCAGT
			QY	4977	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
			Db	525	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
			QY	5037	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			Db	585	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			QY	5097	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			Db	645	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			QY	5157	CTGTTGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			Db	705	CTCTGGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			QY	5217	ATATT-GGAACCTGGGGATGAGAAAGTGTGACATTTGAGATGAGTACAT-GGGA
			Db	765	ATATGGGGACTCTGGGATGAGAAAGTGTGACATTTGAGATGAGTACATGGGA
			QY	5275	GGTCAGACCCCA-CAAACTCTAACTTACAGCTTCAGCCATCATCTCTGCA
			Db	825	GGTCAGACCCCAACCAAACTTACAGCTTCAGCCATCATCTCTGCA
			QY	5334	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG
			Db	885	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG
			QY	5392	CCCGAGGGACCTTACCGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
			Db	945	CCGAGGGATTTTACGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
			Db	1005	CCCTCTCNCCTGAGTAATTAATTGCTGAATTGGACCAATATGAAATCGGATT
			QY	5508	C 5508
			Db	1065	C 1065
			QY	4497	TGGTGAATTCCGGGAGAGATGCTCTGGTACTGCGCTGCTGGAGTTCCA
			Db	105	ATGCGTCTCCGGCTGGCTCTGGCTCTGGCTCTGGAGTTCCA
			QY	4617	ATGTGTCACCGGGAGGGAGGGAGGGCTCTGGCTCTGGAGTTCCA
			Db	165	ATGCGTCTCCGGCTGGCTCTGGCTCTGGCTCTGGAGTTCCA
			QY	4677	CTGTGAGAAATCTCTCTGGCTCAATGACCACTGGGCTCAATTCCCTCACAGGGT
			Db	225	CTGTCAGAAATCTCTCTGGCTCAATGACCACTGGGCTCAATTCCCTCACAGGGT
			QY	4737	GGATGACCGGGAGTGTGGCTCTGGCTCTGGCA
			Db	285	GGATGACCGGGAGTGTGGCTCTGGCA
			QY	4797	CTTCATGGGATCACTGTGGAAGTGTGGCTCTGGCA
			QY	4917	TTTGCTCTACTTGTAGAAAGCTTACCATCAGCTCAGACTATGTCAGT
			QY	4977	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
			Db	525	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
			QY	5037	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			Db	585	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			QY	5097	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			Db	645	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			QY	5157	CTGTTGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			Db	705	CTCTGGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			QY	5217	ATATT-GGAACCTGGGGATGAGAAAGTGTGACATTTGAGATGAGTACAT-GGGA
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			QY	5275	GGTCAGACCCCA-CAAACTCTAACTTACAGCTTCAGCCATCATCTCTGCA
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			Db	885	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG
			QY	5392	CCCGAGGGACCTTACCGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
			Db	945	CCGAGGGATTTTACGGTAATCTGGAAACCATGACAAATCCAGAA-CCCAAGCT
			Db	1005	CCCTCTCNCCTGAGTAATTAATTGCTGAATTGGACCAATATGAAATCGGATT
			QY	5508	C 5508
			Db	1065	C 1065
			QY	4497	TGGTGAATTCCGGGAGAGATGCTCTGGTACTGCGCTGCTGGAGTTCCA
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			QY	4617	ATGTGTCACCGGGAGGGAGGGAGGGCTCTGGCTCTGGAGTTCCA
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			QY	4677	CTGTGAGAAATCTCTCTGGCTCAATGACCACTGGGCTCAATTCCCTCACAGGGT
			Db	225	CTGTCAGAAATCTCTCTGGCTCAATGACCACTGGGCTCAATTCCCTCACAGGGT
			QY	4737	GGATGACCGGGAGTGTGGCTCTGGCTCTGGCA
			Db	285	GGATGACCGGGAGTGTGGCTCTGGCA
			QY	4797	CTTCATGGGATCACTGTGGAAGTGTGGCTCTGGCA
			QY	4917	TTTGCTCTACTTGTAGAAAGCTTACCATCAGCTCAGACTATGTCAGT
			QY	4977	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
			Db	525	GACCTATGCCAATGAAATGATAACACCCATGTTAACGACTCAATATTG
			QY	5037	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			Db	585	CCTCTTGCTGGATGCTTATATGCTCAAGGACTCTGGGATATGAAT
			QY	5097	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			Db	645	CTGGAGAGACATTGATTGCCCATTGAGCACCGCTTCTGCCTTGGCATAGCTT
			QY	5157	CTGTTGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			Db	705	CTCTGGCTGGTGGAACTGAAATCCAGAAGCTGACGGAGATGAAACTCTATTC
			QY	5217	ATATT-GGAACCTGGGGATGAGAAAGTGTGACATTTGAGATGAGTACAT-GGGA
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			QY	5275	GGTCAGACCCCA-CAAACTCTAACTTACAGCTTCAGCCATCATCTCTGCA
			Db	825	GGTCAGACCCCAACCAAACTTACAGCTTCAGCCATCATCTCTGCA
			QY	5334	GATGTTGCTGTAGCGGA-TTGGGAGGATACACAGCCATCAGTC-TTATGCAATGGACG

Clone distribution: MGIC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLL at: <http://image.llnl.gov>
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FEATURES
source
Location/Qualifiers
1. .903
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/note="Organ: skin; Vector: pCMV-SPORT5; Site: NotI; Site2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life

1128

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QY	5749	CCAGAAGGCAATGACCCATGGACATAACCGGAATCTACATGGTCCCTTATACCA	5808	Db	68	CTAACCTRACTTTCAGCAAGCATACCATCAGTCAGACTATGTCATCCCATAGGACCA	127
Db	660	CCAGAAGGCAATGACCCATGGACATAACCGGAATCTACATGGTCCCTTATACCA	719	QY	4983	TGCCCCAAATGAAAATSGATCAACCCATGTTAAGACATCAATTATGACCTT	5042
QY	5809	CTGTCAGAATGCTGTTTATTCATCCAAAGATCTGGCTATGCAATAGCTAT	5868	Db	128	TGCCCCAAATGAAAATSGATCAACCCATGTTAAGACATCAATTATGACCTT	187
Db	720	CTGTCAGAATGCTGTTTATTCAT-CHAGGATCTGGCTATGCAATAGCTAT	778	QY	5043	TGCTGTGATGCAATATAGTCAGATGATCAGTCACTGCTGGGATATGAATCTGAG	5102
QY	5869	CTACAGAGTTCAAGCCAGACTCTTCAGAAGTACATTAAGCTATTTGGACAG-C	5927	Db	188	TGCTGTGATGCAATATAGTCAGATGCACTGCTGGGGATCTGAAATCTGGAG	247
Db	779	CTACAGAGTTCAAGCCAGACTCTTCAGAAGTACATTAAGCTATTTGGACAG-C	838	QY	5103	AGACATGATTGCCCCATGAGCACAGCTTTCGCGCTTGAGCATGACTCTTCTG	5162
QY	5928	GAGTCGGATCTGGCTATGGCTCTGGCCGCGCA--TGGTAAGGGCGTCTCACTGC	5984	Db	248	AGACATGATTGCCCCATGAGCACAGCTTTCGCGCTTGAGCATGACTCTTCTG	307
Db	839	GAGTCGGATCTGGCTATGGCTCTGGCCGCGNAATGGAAGGGCCCTCTCACTGG	898	QY	5163	GGCTGGGACAGAAATCCAGAAGCTGACAGGAGTGAAGACTCAGTCCATATG	5222
QY	5985	CC 5986	Db	308	GGCTGGGACAGAAATCCAGAAGCTGACAGGAGTGAAGACTCAGTCCATATG	367	
Db	899	CC 900	Db	368	GGACTGGGGATGCAAAAGTGTGACATTGCACTGGATGATGAGTACAGGAGGTCAGCA	427	
RESULT 8							
LOCUS	BQ424642	926 bp mRNA linear EST 23-MAY-2002	QY	5283	CCGCCAAATCTTAACCTACTCAGCCAGCATCTTCTCTCTGGAGAATGCTG	5342	
DEFINITION	AGENCOURT_7926673 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6160409		Db	428	CCGCCAAATCTTAACCTACTCAGCCAGCATCTTCTCTCTGGAGAATGCTG	487	
ACCESSION	5', mRNA sequence.		QY	5343	TAGCCGATGGAGGAGTACAACAGCCATCAGCTTATGCAATGGAAAGGCCAGGGACC	5402	
VERSION	BQ424642.1	EST.	Db	488	TAGCCGATGGAGGAGTACAACAGCCATCAGCTTATGCAATGGAAAGGCCAGGGACC	547	
KEYWORDS			Db	5403	TTTACGGCTAACTCTGAAACATGACAATCGAGCACTGCTGCTGAGATGCTG	5462	
SOURCE	Homo sapiens (human)		Db	548	TTTACGGCTAACTCTGAAACATGACAATCGAGCACTGCTGCTGAGATGCTG	607	
ORGANISM			QY	5463	TTATGTGAAATTGCTGTAGTTGACCAATATGATCTGTTCTGATGAAAGCTG	5522	
REFERENCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		Db	608	TGATGTGAAATTGCTGTAGTTGACCAATATGATCTGTTCTGATGAAAGCTG	666	
AUTHORS	1. (bases 1 to 926)		QY	5523	CAATTAGCTTAAAGAACATGCAATTCAGAACCCAGGCTCCCTCTGAGC	5582	
TITLE	NIH-MGC http://mgc.ncbi.nih.gov/		Db	667	CAATTAGCTTAAAGAACATGCAATTCAGAACCCAGGCTCCCTCTGAGC	726	
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		QY	5583	TGCTCTCAAGAGCGTGTGACATCTGCTGACATCTATGTAATGAGCAATGT-CCC	5641	
COMMENT	Unpublished (1999)		Db	727	TGCTCTCAAGAGCGTGTGACATCTATGTAATGAGCAATGT-CCC	786	
	Contact: Robert Strauberg, Ph. D.		QY	5642	AGTAGTACGGGATCTGCCAACATGCTCTCTCTCCATGTCAGTTGTCAGTC	5698	
	Email: cgsbps-r@mail.nih.gov		Db	787	AGTAGTACGGGATCTGCCAACATGCTCTCTCTCCATGTCAGTTGTCAGTC	846	
	Tissue Procurement: ATCC/DCTD/DPMP		QY	5699	GAATTGAGGAGTGCCTCCGAAGGACCGTCC- TCTTCAGAAGTTATCCAGAAGC	5756	
	cDNA Library Preparation: Life Technologies, Inc.		Db	847	AAATTGAGGAGTGCCTCCGAAGGACCGTCC- TCTTCAGAAGTTATCCAGAAGC	906	
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)		QY	5757	CAATGCCCATGGACATA 5776		
	DNA Sequencing by: Agencourt Bioscience Corporation		Db	907	CATGCAACCATGGACATA 926		
	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov						
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	/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SAI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2 kb. Library constructed by Life Technologies."						
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Query Match	12.8%; Score 817.4; DB 13; Length 926;						
Best Local Similarity	96.5%; Pred. No. 1; se-223; Mismatches 24; Indels 8; Gaps 5;						
QY	4863	ACTCTGGAGAGAACATCTTGATTTGAGTGGCTGCCCAAGAGAGAACATTGTC	4922	Db	4924713	BO424713 AGENCOURT_7926435 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6160418	
Db	9	ACCTGGAGAGAACATCTTGATTTGAGTGGCTGCCCAAGAGAGAACATTGTC	67	QY	4924713.1	GI:21120028	
ORGANISM							
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.						

		COMMENT
QY	4557 GACCTCCGCTGGCCATTTCCTAGCCCTGTCCTCTTAAGAACCTGATSGAGAGGA	4616
Db	96 GACCTCCGCTGGCCATTTCCTAGCCCTGTCCTCTTAAGAACCTGATSGAGAGGA	155
QY	4617 ATGGTGTCCACCGGGAGACGGGACAGAGTCCTGTCGCCAGCTTCAGGAGGGTC	4676
Db	156 ATGGTGTCCACCGGGAGACGGGACAGAGTCCTGTCGCCAGCTTCAGGAGGGTC	215
QY	4677 CTGTCAGAAATCCTCTGTCCTAGAACACTGGGCTCAATTCCCTACAGGGT	4736
Db	216 CTGTCAGAAATCCTCTGTCCTAGAACACTGGGCTCAATTCCCTACAGGGT	275
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Db	756 CATTATGGCTGGGGATGCCAGAAAGTGTGACATTGCAAGATGAGTACAT-GGGA	815
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QY	5335 ATTTCTGTPGCCATTGGAGGATAC	5361
Db	876 ATTTCTGTPGCCATTGGAGGATAC	902
RESULT 11		
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DEFINITION 602596831 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4708629		
ACCESSION BG576440		
VERSION BG576440.1		
KEYWORDS EST.		
SOURCE Homo sapiens (human)		
ORGANISM Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE 1 (bases 1 to 965) NIH-MGC http://mgc.nci.nih.gov/.		
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL Unpublished (1999)		
	COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgrabs_r@mail.nih.gov
		Tissue Procurement: DCTN/DRP
		cDNA Library Preparation: Life Technologies, Inc.
		cDNA Library Arrived by: The I.M.A.G.E. Consortium (LNU)
		DNA Sequencing by: Incyte Genomics, Inc.
		Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNU at: http://image.lnl.gov
		Plate: LNU10580 row: f column: 22
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		Site 2: Sali; Cloned unidirectionally; oligo-dt primed.
		Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.
		Note: this is a NIH_MGC Library."
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	Query Match	12.3%; Score 787.6; DB 12; Length 965;
	Best Local Similarity	94.1%; Pred. No. 6.3e-215;
	Matches	886; Conservative 0; Mismatches 44; Indels 12; Gaps 6;
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	QY	5228 GCGGGATGTCGACAAAGTGCACATTGTCACAGATGATGTCATGGGGTCAGACCCCA
	Db	23 GCGGGATGTCGACAAAGTGCACATTGTCACAGATGTCATGGGGTCAGACCCCA
	QY	5288 CAATCTTACTACTAGCCAGCTTCAATTCTCTCTGGCAATGTCGACCC
	Db	83 CAATCTTACTACTAGCCAGCTTCAATTCTCTCTGGCAATGTCGACCC
	QY	5348 GATTGGGGAGTACACAGCCATGCTTGTGCAATTGGAAACGCCAGGGACCTTAC
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	QY	5408 GCGGTAATCCCGAAACCATGCAAACTTCAAGAACCCCCAGCTCCCTTCAGCTGAG
	Db	203 GCGGTAATCCCGAAACCATGCAAACTTCAAGAACCCCCAGCTCCCTTCAGCTGAG
	QY	5468 TAGATTTCGTCGAGTTGACCAATATGAACTTGGTCCTCTGGATTAAGCTGCCATT
	Db	263 TAGATTTCGTCGAGTTGACCAATATGAACTTGGTCCTCTGGATTAAGCTGCCATT
	QY	5528 TCGCTTTAGAAATACHTGGAGGATTTGCTAGTCCTACTGGATACGGATGCC
	Db	323 TCGCTTTAGAAATACHTGGAGGATTTGCTAGTCCTACTGGATACGGATGCC
	QY	5588 CTCAAACAGCATGCAACATGCTTCGACATATGAACTGTCCTCCAGGTAC
	Db	383 CTCAAACAGCATGCAACATGCTTCGACATATGAACTGTCCTCCAGGTAC
	QY	5648 AGGGATTCGCAACGATCTTCTTCACATGATGTCACATGTCAGTCAGTCAGTTTG
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	QY	5708 AGGAGTGGCTCGAGGACCTCTCTTCAGAAAGTTTACGAGGCCATGACCCA
	Db	503 AGGAGTGGCTCGAGGACCTCTCTTCAGAAAGTTTACGAGGCCATGACCCA
	QY	5768 TGGACATAACCGGGATTCATGGCTTCCTTACACTGTGAGAATGGTA-T
	Db	563 TGGACATAACCGGGATTCATGGCTTCCTTACACTGTGAGAATGGTA-T
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Db	623	TTCTTATTTCATCCAAAGATCTGGCTATGACTATAGCTATCAAGATTAGACCCA	682	QY	1615	AGCTCTGGTTACTCATATACTTGTAGATTAACTCTATTAAAG	1674
QY	5887	GACTCTTCAAGACTACATTAAGCTCTATTGGAACACAGGAGCTGGATCTGTCATGG	5946	Db	794	AGACCAAGTTACTCATATACTTGTAGATTAACTCTATTAAAG	735
Db	683	GACTCTTCAAGACTACATTAAGCTCTATTGGAACACAGGAGCTGGATCTGTCATGG	742	QY	1675	GATCTAGTGAAAGATCTCTTGTATAUTCTCATGACCAAATCCCTAACGAGTTTC	1734
QY	5947	CTCCCTGGGGGGG-GATGTTAGGGGCTCTACTGCCTGTTGGAGACAGCAGTCGGATCTGTCATGG	6005	Db	734	GATCTAGTGAAAGATCTCTTGTATAUTCTCATGACCAAATCCCTAACGAGTTTC	675
Db	743	CTCCCTGGGGGGGAAAGCTTAGGGGCTCTACTGCCTGTTGGAGACAGCAGTCGGATCTGTCATGG	802	QY	1735	GTTCACATGAGCTCAAGCCCTTAGAAAAGATCAAGGATCTCTTGAGATCCTT	1794
QY	6006	CTGCTGTTGCTGCAAGAGA---AGGAGCTCTGAAAGAAAGCAGCACTC---C	6058	Db	674	GTTCACATGAGCTCAAGCCCTTAGAAAAGATCAAGGATCTCTTGAGATCCTT	615
Db	803	CTGCTGTTGCTGCAAGAGAAGACGCCCTTGAGAAAAGCAGCACTCCTC	862	QY	1795	TCTCGCGTAACTGCTGCTGAAAGAAACCCGCTACAGGGTGTGTTTT	1854
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Db	863	ATGGCGCAAGAAGGATACCCACAGCTGATCAGAGCCATATAACAGGCTTAAGGC	922	QY	1855	GCCGGATCAGAGCTACCAACTCTTTCGGAAGGTAAGTACTGCTTCAAGAGCAGAT	1914
QY	6116	CAATAGAGTGGCCAAAGACCTGACTCTAACTCAA	6157	Db	554	GCCGGATCAGAGCTACCAACTCTTTCGGAAGGTAAGTACTGCTTCAAGAGCAGAT	495
Db	923	AATTGAGGTAGGCCAAAAGCCTGACTACTTAACCTCAA	964	QY	1915	ACCAATACTGTTCTAGTGTAGCTAGTAGGCCACCTCTGAGAAACTCTGAGC	1974
RESULT	12			Db	494	ACCAATACTGTTCTAGTGTAGCTAGTAGGCCACCTCTGAGAAGCTGAGCTGAGC	435
LOCUS	AJ281480	1004 bp mRNA linear EST 30-JUN-2000		QY	1975	ACCCCTACATACCTCCGCTCGTAATCTGTGTTACAGCTGGCTGCTGCAGTGGATAA	2034
DEFINITION	4A3A-P4G8-F	Anopheles gambiae immune competent 4A3A	Anopheles	Db	434	ACCCCTACATACCTCCGCTCGTAATCTGTGTTACAGCTGGCTGCTGCAGTGGATAA	375
ACCESSION	AJ281480	gambiae cDNA clone 4A3A-P4G8, mRNA sequence.		QY	2035	GTGGTGTCTTACCGGGTTGGACTCAACAGATAAGTGTACCGGATAAGGGCAACGGT	2094
VERSION	AJ281480.1	GI:929360		Db	374	GTCTGTCTTACCGGGTTGGACTCAACAGATAAGTGTACCGGATAAGGGCAACGGT	315
KEYWORDS	EST.			QY	2095	CTGAGCCGGGGTCTGTCACAGCAGCCAGCTGGAGGAACTACCGAACCTACACGACTG	2154
SOURCE	Anopheles gambiae (African malaria mosquito)			Db	314	CTGAGCCGGGGTCTGTCACAGCAGCCAGCTGGAGGAACTACCGAACCTACACGACTG	255
ORGANISM	Anopheles gambiae	(African malaria mosquito)		QY	2155	ATACCTACAGCGCTGAGCTATGAGAAAGGCCAGCTTCCGAGGGAAAGGGAGCAG	2214
REFERENCE	Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C., Donohue, M., Schultz, J., Benes, V., Bork, P., Ansorge, W., Soares, M.B. and Kafatos, F.C.			Db	254	ATACCTACAGCGCTGAGCTATGAGAAAGGCCAGCTTCCGAGGGAAAGGGAGCAG	195
AUTHORS	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines			QY	2215	GTATCCGTAAGGGCTGTCGACAGCCAGCTGGAGGAACTACCGAACCTACACGACTG	2274
TITLE	Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)			Db	194	GTATCCGTAAGGGCTGTCGACAGCCAGCTGGAGGAACTACCGAACCTACACGACTG	135
JOURNAL	MEDLINE			QY	2275	CGCTGTGATCTTATGCTCTCGCTGGTTCCACCTCTGACTTCTGGCTGATTT	2334
PUBMED	10841561			Db	134	CGCTGTGATCTTATGCTCTCGCTGGTTCCACCTCTGACTTCTGGCTGATTT	75
COMMENT	Contact: Dimopoulos G			QY	2335	GTATCCGTAAGGGCTGTCGACAGCCAGCTGGAGGAACTACCGAACCTACACGACTG	2394
	Fotis C, Kafatos C			Db	74	GTATCCGTAAGGGCTGTCGACAGCCAGCTGGAGGAAAGGGAGCAG	15
FEATURES	European Molecular Biology Laboratory			QY	2395	GTTCCTGGCTTTT 2418	
SOURCE	Meyerhofstrasse 1, 69117 Heidelberg, Germany.			Db	14	GTTCCTGGCTTTT 1	
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	/mol_type="mRNA"			ACCESSION	AJ281449	gambiae cDNA clone 4A3A-P4D5, mRNA sequence.	
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TITLE	Anopheles gambiae pilot gene discovery project: identification of mosquito innate immunity genes from expressed sequence tags generated from immune-competent cell lines
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
MEDLINE	20300950
PUBMED	10841561
COMMENT	Contact: Dimopoulos G Fotis C. Kafatos laboratory European Molecular Biology Laboratory Meyerhofstrasse 1, 69117 Heidelberg, Germany. Location/Qualifiers
FEATURES	1. .800 /organism="Anopheles gambiae" /mol_type="mRNA" /strain="4A x/x" /db_xref="taxon:7155" /clone="4A3A-P4D5" /cell_line="immune competent 4A3A" /lab_host="E. coli DH10B" /clone_lab="Anopheles gambiae immune competent 4A3A" /note="Vector: pT7TBD-Pac (Pharmacia) with a modified polylinker; Site 1: ECORI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Ronald, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."
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Db	560 TCTTTTCGAGGTAATCTGCTTCAAGCAGCCGAATACCAAAATCTGTCTTCTAGT 501
Db	1936 CTAGCGTAGTGTGACCACTCTAGAACTCTGAGCACCCATACCTCTCT 1995
Db	500 GTAGCGTAGTGTGACCACTCTAGAACTCTGAGCACCCATACCTCTCT 441
QY	1996 GCTAAATCTGTTACCTGAGCTGGCTGCTGCAGTGGCGATAAGTGTGTCTACCGGTGGA 2055
Db	440 GCTAAATCTGTTACCTGAGCTGGCTGCTGCAGTGGCGATAAGTGTGTCTACCGGTGGA 381
OY	2056 CTCAGACGATAGTTCGGATAGCGCGAGGGTCGGGTCAGCGGGGTGGCAC 2115
Db	380 CTCAGACGATAGTTCGGATAGCGCGAGGGTCGGGTCAGCGGGGTGGCAC 321
OY	2116 ACAGCCAGCTGGAGGAGACCTACACGGACTAGATACTCAGGGTAGCTG 2175
Db	320 ACAGCCAGCTGGAGGAGACCTACACGGACTAGATACTCAGGGTAGCTG 261
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JOURNAL	NIH_MSC
COMMENT	unpublished (1999)
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AUTHORS	NIH_MSC http://mgc.nci.nih.gov/.
VERSION	BII79860
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AUTHORS	1
DEFINITION	AGECOURT_811031_NIH_MSC_112 Homo mRNA 939 bp
TITLE	mRNA
JOURNAL	linear EST 04-SEP-2002 IMAGE:6266889
COMMENT	Contract: Robert Strausberg, Ph.D. Email: cbrapsr@mail.nih.gov Tissue Procurement: bcrmp@dtp cDNA Library Preparation: Rubin Laboratory DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the T.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LUCM2436 Row: F column: 10 High quality sequence stop: 606.
FEATURES	location/qualifiers
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ORIGIN	
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Best Local Similarity	93.0%; Pred. No. 1.7e-210;
Matches	863; Conservative 0; Mismatches 56; Indels 9; Gaps 5;
OY	5446 AGCTCCCTCTCTAGCTGATGAGTTTCCTGAGTTGACCCATATGATCTGT 5505
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FEATURES	SOURCE	REFERENCE
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Db	61 TCCATGATAAAGCTGCCATTCACTGAGTAAATACACTGAGGATTGCTGAGTCCA	NIH-MGC http://mgc.nci.nih.gov/ , National Institutes of Health, Mammalian Gene Collection (MGC)
Qy	5566 CTTACTGGATAGGGATGCTCTCAAAGGCTGAGGATGCTGAGGATTCACATGAGATTC	120 Unpublished (1999)
Db	121 CTTACTGGATAGGGATGCTCTCAAAGGCTGAGGATGCTGAGGATTCACATGAGATTC	Contact: Robert Strausberg, Ph.D.
Qy	5626 AATGGACAGATGCTCAGGATGCTCTCAAAGGCTGAGGATGCTGAGGATTCACATGAGATTC	Email: cggpbs-f@mail.nih.gov
Db	181 AATGGACAGATGCTCAGGATGCTCTCAAAGGCTGAGGATGCTGAGGATTCACATGAGATTC	5625
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Qy	6220 TTGTGACCTTATAGAAAGTAGCTGCTGGSCAAAGGCCTGACTCTAATCTAAAGTAATG	6277
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Qy	6278 GTCTGTCT-GTTTCACTGCTTACATTTCCCTAACCCATAGTCAAGA	6336
Db	841 GCCTTGCTGTTTCACTGCTTACATTTCCCTAACCCATAGTCAAGA	900
Qy	6337 AAGGATGCTTGTGAAATGAGGAACTG 6364	
Db	901 AGGAAGGCTATGCCATTGGGAATG 928	
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LOCUS	AGENCONT_8106643	5' mRNA sequence.
DEFINITION		
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VERSION	BU191334.1	GI:22705318
KEYWORDS	EST.	
SOURCE	Home sapiens (human)	
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	

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Oy	5050	ATGCATATTATGTCATGCTGCACTGCTTGCGATGTAATGAAATCTGGAGACATT	5109
Db	548	ATGCATATTATGTCATGCTGCACTGCTTGCGATGACTGCTTGCGGGATCTGAATCTGGAGAGATT	607
Oy	5110	GATTTGCCATGAGCCAGCTTTCGCTTGCGATGACTGCTTGCGGGATCTGAATCTGGAGAGATT	5169
Db	608	GATTTGCCATGAGCCAGCTTTCGCTTGCGATGACTGCTTGCGGGATCTGAATCTGGAGAGATT	667
Oy	5170	GACAAGAAATCGAGAGCTGAGAGGAGATGAAACTCACTATCCATATGGACTGG	5229
Db	668	GAACAGAAATCCAGAAGCTGAGAGGAGATGAACTCACTATCCATATGGACTGG	727
Oy	5230	CGGGATGCCAAAGTGTGACATTTGCAGATGA - GTCACATGGAGGTAGACCCCCA	5287
Db	728	CGGGATGCCAAAGTGTGACATTTGCAGATGAAGTACTCGGGAGGGTAGCACCCA	787
Oy	5288	CAATCCAACTT	5300
Db	788	CAATCCAACTT	800

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 Job time : 14710 secs